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OM protein - protein search, using sw model

Run on: September 9, 2005, 15:56:35 ; Search time 92.1 Seconds
(without alignments)
25.196 Million cell updates/sec

Title: US-10-032-037C-8

Perfect score: 29

Sequence: 1 MRAPIV 6

Scoring table: BLOSUM62

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_16Dec04:*

1: geneseqp19808:.*
2: geneseqp19808:.*
3: geneseqp20008:.*
4: geneseqp20018:.*
5: geneseqp20028:.*
6: geneseqp20038:.*
7: geneseqp20038:.*
8: geneseqp20048:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	6	AAW77197	Abg77197 Pharmacu
2	29	100.0	6	ABG78133	Abg78133 Human Fv
3	29	100.0	6	ABG91824	Abg91824 Human ant
4	29	100.0	6	AD128369	Ad128369 Human CDR
5	29	100.0	6	ADJ57364	Adj57364 P-selecti
6	29	100.0	246	ABG78329	Abg78329 Human Fv
7	29	100.0	246	ABG92026	Abg92026 Antibody
8	29	100.0	256	ABG78334	Abg78334 Human Fv
9	29	100.0	256	ABG92025	Abg92025 Antibody
10	29	100.0	277	ABG78150	Abg78150 Human ant
11	29	100.0	277	ABG78150	Abg78150 Human Fv
12	29	100.0	277	ABG91841	Abg91841 Human ant
13	29	100.0	277	AD128366	Ad128366 Human bcf
14	29	100.0	278	AD128367	Ad128367 Human bcf
15	29	100.0	280	AD128368	Ad128368 Human bcf
16	29	100.0	280	ADJ57363	Adj57363 P-selecti
17	29	100.0	442	ADN25218	Adn25218 Bacterial
18	29	100.0	464	ABG78151	Abg78151 Human Fv
19	29	100.0	464	ABG92021	Abg92021 Antibody
20	29	100.0	464	ABG91842	Abg91842 Human ant
21	29	96.6	133	AAU42688	Aau42688 Propionib
22	29	96.6	133	ABM39207	Abm39207 Propionib
23	29	96.6	438	AAE14569	Aae14569 Human rho
24	29	96.6	438	ADA13449	Ada13449 Human rho
25	29	96.6	438	ADA13415	Ada13415 Human rho

26	28	96.6	438	7	ADG47134	Adg47134 Human rho
27	28	96.6	438	7	ADG47100	Adg47100 Human rho
28	28	96.6	470	7	ADA13459	Ada13459 Mouse rho
29	28	96.6	470	7	ADG47144	Adg47144 Mouse rho
30	28	96.6	541	4	AAAG90242	Aag90242 C glutami
31	28	96.6	973	7	ABO75198	AbO75198 Pseudom
32	27	93.1	116	4	AAU44808	Aau44808 Propionib
33	27	93.1	116	6	ABM41327	Abm41327 Propionib
34	26	89.7	33	4	AAW82945	Aaw82945 Human imm
35	26	89.7	58	4	AAU56719	Aau56719 Propionib
36	26	89.7	58	6	ABM53238	Abm53238 Propionib
37	26	89.7	226	5	ABP73581	Abp73581 Candida a
38	26	89.7	286	4	AAAG98915	Aag98915 E. coli g
39	26	89.7	286	6	ABU15292	Abu15292 Protein e
40	26	89.7	286	8	ADS45133	Ads45133 Bacterial
41	26	89.7	290	6	ABU28269	Abu28269 Protein e
42	26	89.7	350	2	AAAY35225	Aay35225 Chlamydia
43	26	89.7	405	7	ADC87283	Adc87283 Human GPC
44	26	89.7	477	7	ABO62389	AbO62389 Klebsiell
45	26	89.7	1449	4	ABB66060	Abb66060 Drosophila

ALIGNMENTS

RESULT 1
AAW77197 standard; peptide; 6 AA.
XX
XX AAW77197;
AC
XX
DT 23-NOV-1998 (first entry)
XX
XX
DE Pharmaceutically active peptide 38.
XX
XX Pharmaceutically active peptide; target; organ; lymphocyte; treatment;
KM pharmaceutical agent; disease; radioactive isotope; imaging agent.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX
PN WO9839469-A1.
XX
XX 11-SEP-1998.
PD
XX
XX 04-MAR-1998; 98WO-US004188.
PF
XX
PR 04-MAR-1997; 97US-0039509P.
PR 04-MAR-1997; 97US-00810074.
XX
XX (BIOT-) BIO-TECHNOLOGY GENERAL CORP.
XX
XX Panet A, Hagai Y, Lazarovits J, Nimrod A, Vogel T, Levanon A;
PI Zeelon E, Belkind A, Golan I;
XX
XX WPI; 1998-495863/42.
XX
XX
XX New peptide(s) binding targets in organs and lymphocytes - used for the
PT targeted delivery of toxins, anti-cancer drugs and cardiovascular agents
PT to arteries, veins, placenta, liver.
XX
XX
XX Claim 76; Page 99; 114pp; English.
XX
XX Sequences shown in AAW77160 to AAW77214 and AAW79167 represent non-
CC naturally-occurring pharmaceutically active peptides. These novel
CC peptides specifically bind to undetermined and determined targets in
CC various organs and in lymphocytes. The peptides can be used in
CC compositions, where they can be linked to pharmaceutical agents, to treat
CC various diseases and conditions. The peptides or chimeric polypeptides
CC comprising these pharmaceutically active peptides and a second peptide
CC may be labelled with a marker (radioactive isotope, etc) to form an
CC imaging agent. This agent is used to bind an organ so that the organ can
CC be imaged

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 29; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
 1 MRAPVI 6

Db 1 MRAPVI 6

RESULT 2
 ABG78133
 ID ABG78133 standard; peptide; 6 AA.
 XX ABG78133;
 AC ABG78133;
 XX
 DT 15-NOV-2002 (first entry)
 XX
 DE Human Fv molecule hypervariable region related peptide #8.
 XX
 KW Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
 KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
 KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200259264-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 31-DEC-2001; 2001WO-US049440.
 XX
 PR 29-DEC-2000; 2000US-00751181.
 XX
 PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
 XX
 PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
 PI Plakein D, Peretz T;
 XX
 DR WPI; 2002-619166/66.
 XX
 PT Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
 PT or fragment, or construct of fragment with enhanced binding
 PT characteristics so as to selectively bind target cell in favor of other
 PT cells.
 XX
 PS Claim 2; Page 76; 232pp; English.
 XX
 CC The invention relates to a peptide or polypeptide comprising an Fv
 CC molecule, a construct or fragments of a construct of a fragment with
 CC enhanced binding characteristics which selectively and/or specifically
 CC binds to a target cell in favour of other cells, where binding is
 CC primarily determined by a first hypervariable region and Fv is a single
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
 CC association with or attached, coupled, combined, linked or fused to a
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where
 CC the medicament has activity against a diseased cell, preferably a cancer
 CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
 CC composition for use in inhibiting the growth of a diseased or cancer
 CC cell. This sequence represents a human Fv molecule hypervariable region
 CC related peptide of the invention
 XX
 SQ Sequence 6 AA;

Query Match 100.0%; Score 29; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6

Db 1 MRAPVI 6

RESULT 3
 ABG91824
 ID ABG91824 standard; peptide; 6 AA.
 XX ABG91824;
 AC ABG91824;
 XX
 DT 04-DEC-2002 (first entry)
 XX
 DE Human antibody fragment #8.
 XX
 KW Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
 KW metastasis; hypervariable region; autoimmune disease; thrombosis;
 KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
 KW myocardial infarction; retinopathic disease; abnormal platelet function;
 KW sulphated tyrosine-dependent protein-protein interaction.
 XX
 OS Homo sapiens.
 XX
 PN WO200253700-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 31-DEC-2001; 2001WO-US049442.
 XX
 PR 29-DEC-2000; 2000US-00751181.
 XX
 PR 29-DEC-2000; 2000US-0258948P.
 XX
 PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
 XX
 PI Lazarovits J, Hagai Y, Plakein D, Vogel T, Nimrod A, Mar-Haim H;
 PI Szanton E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
 XX
 DR WPI; 2002-674776/72.
 XX
 PT Novel isolated epitope present on cancer cells and important in
 PT physiological phenomena such as cell rolling, metastasis and
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular
 PT diseases, and cancer.
 XX
 PS Claim 1; Page 228; 0pp; English.
 XX
 CC The invention relates to an isolated epitope present on cancer cells and
 CC important in physiological phenomena such as cell rolling, metastasis and
 CC inflammation, where the epitope is capable of being bound by an antibody,
 CC its antigen-binding fragment or its complex comprising at least one
 CC antibody or its binding fragment having a first hypervariable region. The
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing
 CC mortality of tumour or leukaemia cells, for increasing the susceptibility
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-
 CC leukaemia agents, or for decreasing the number of tumour or leukaemia
 CC cells in a patient, or in the manufacture of a medicament for the above
 CC mentioned purposes. The epitopes are useful for diagnosing and treating
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
 CC diseases, cardiovascular diseases such as myocardial infarction,
 CC retinopathic diseases and other diseases mediated by abnormal platelet
 CC function and diseases caused by sulphated tyrosine-dependent protein-
 CC protein interactions. This sequence represents a human antibody fragment
 CC of the invention
 XX
 SQ Sequence 6 AA;

Query Match 100.0%; Score 29; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
 DB 1 MRAPVI 6

RESULT 4

AD128369
 ID AD128369 standard; peptide: 6 AA.

AC AD128369;

DT 06-MAY-2004 (first entry)

DE Human CDR3 peptide, used in therapeutic composition.

XX Human; antibody; scFv; complementarity determining region; drug delivery;
 XX cancer; therapy.

OS Homo sapiens.

PN W02004002528-A1.

PD 08-JAN-2004.

PF 30-JUN-2003; 2003WO-US020604.

PR 01-JUL-2002; 2002US-00189025.

XX (SAVI-) SAVIENT PHARM INC.

PI Lazarovits J, Nimrod A, Hoch-Mar-Chaim H, Levanon A;

PT WPI; 2004-099189/10.

XX Composition comprising an agent and/or antibody or its fragment, useful
 PT for treating auto-immune disease, thrombosis, restenosis, metastasis, or
 PT for inhibiting growth and/or replication of tumor cells or leukemia
 cells.

PS Claim 14; SEQ ID NO 4; 58pp; English.

XX The present sequence is that of a human antibody complementarity
 CC determining region 3 (CDR3). The invention relates to compositions
 CC utilising an agent and an antibody or its fragment. The agent is a toxin,
 CC radioisotope or pharmaceutical agent such as doxorubicin. It is complexed
 CC or combined with or conjugated to the antibody or its fragment. The
 CC antibody may have a first hypervariable region comprising the present
 CC sequence. The agent and/or antibody can be present in the composition is
 CC a sub-clinical amount, i.e. less than the amount generally found to be
 CC clinically effective when the agent is administered alone.
 CC Composition is used in claimed methods of: inhibiting cell rolling,
 CC inflammation, thrombosis, restenosis, metastasis, the growth and/or
 CC replication of tumour cells or leukaemia cells, an increase in number of
 CC tumour or leukaemia cells, cell-cell, cell-matrix, platelet-matrix,
 CC platelet-platelet and/or cell-platelet complex formation, aggregation or
 CC adhesion; increasing the mortality rate of tumour or leukaemia cells, the
 CC susceptibility of disease cells to damage by anti-disease agents, and the
 CC susceptibility of tumour or leukaemia cells to damage by anti-cancer
 CC agents; and ameliorating the effects of a disease, preventing a disease,
 CC treating a disease or inhibiting the progress of a disease.

XX Sequence 6 AA;

QY Query Match 100.0%; Score 29; DB 8; Length 6;

Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
 DB 1 MRAPVI 6

RESULT 5

ID ADJ57364
 ID ADJ57364 standard; peptide: 6 AA.

AC ADJ57364;

DT 06-MAY-2004 (first entry)

DE P-selectin glycoprotein ligand-1-binding scFv antibody fragment L32 CDR3.

XX P-selectin glycoprotein ligand-1; PSGL-1; antibody; scFv; cytostatic;
 XX antiinflammatory; immunosuppressive; complementarity determining region;
 XX human.

OS Homo sapiens.

PN W02004003166-A2.

PD 08-JAN-2004.

PF 30-JUN-2003; 2003WO-US020602.

PR 01-JUL-2002; 2002US-00189032.

XX (SAVI-) SAVIENT PHARM INC.

PI Levanon A, Ben-Levy R, Plaksin D, Stanton E, Hagai Y;

PT Hoch Mar-Chaim H;

PT WPI; 2004-203378/19.

XX Novel antibody or its fragment that binds to an epitope of P-selectin-
 PT glycoprotein ligand-1, useful for diagnosing/prognosing inflammation,
 PT infection, auto-immune disease, metastasis, tumor/leukemia cell in
 PT patient.

PS Claim 2; SEQ ID NO 2; 106pp; English.

XX The present sequence is that of the heavy chain complementarity
 CC determining region 3 (CDR3) of L32 ADJ57363, an scFv antibody fragment
 CC that binds P-selectin glycoprotein ligand-1 (PSGL-1). L32 was identified
 CC by screening a phage library, which had diversity only in the heavy chain
 CC CDR3 regions, against a leukaemia cell surface determinants, wherein the specific
 CC receptor was not previously known or characterised. The invention relates
 CC to an antibody or its fragment having the binding capabilities of L32 and
 CC comprising at least one of the heavy chain CDRs of L32. Such antibodies
 CC can be used in therapeutic, diagnostic, prognostic and staging methods.
 CC Pharmaceutical compositions comprising such antibodies are used to treat
 CC conditions related to: inhibiting or treating cell rolling, inflammation,
 CC autoimmune disease, infection (e.g. HIV infection), metastasis, and
 CC growth and/or replication of tumour cells; increasing the mortality of
 CC tumour cells; inhibiting growth and/or replication of tumour cells;
 CC inhibiting growth and/or replication of leukaemia cells; increasing the
 CC mortality rate of leukaemia cells; altering the susceptibility of
 CC diseased cells to damage by anti-disease agents; increasing the
 CC susceptibility of tumour cells to damage by anti-cancer agents;
 CC increasing the susceptibility of leukaemia cells to damage by anti-
 CC leukaemia agents; inhibiting increase in number of tumour cells in a
 CC patient; decreasing the number of tumour cells in a patient; inhibiting
 CC increase in number of leukaemia cells in a patient; and decreasing the
 CC number of leukaemia cells in a patient. Other methods are provided to
 CC induce antibody-dependent cell-mediated cytotoxicity or stimulate natural
 CC killer or T cells using the antibodies. A method of purging tumour cells
 CC from a patient involves incubating the cells with the antibody.

XX Sequence 6 AA;

QY Query Match 100.0%; Score 29; DB 8; Length 6;

Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
 DB 1 MRAPVI 6

Db 1 MRAPI 6

RESULT 6
ABG78329

ID ABG78329 standard; protein; 246 AA.

XX
XX
AC ABG78329;
XX
DT 15-NOV-2002 (first entry)
XX
DE Human Fv molecule hypervariable region related peptide #204.
XX
XX Human; Fv molecule; hypervariable region; single chain Fv; cytototoxic;
KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukemia; adenoma;
KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukemia.
XX
OS Homo sapiens.
XX
PN WO200259264-A2.
XX
PD 01-AUG-2002.
XX
PF 31-DEC-2001; 2001WO-US049440.
XX
PR 29-DEC-2000; 2000US-00751181.
XX
PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX
PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Stanton E, Levanon A;
PI Plaksin D, Peretz T;
DR WPI; 2002-619166/66.
XX
XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
PT or fragment, or construct of fragment with enhanced binding
PT characteristics so as to selectively bind target cell in favor of other
PT cells.
XX
PS Disclosure; Page 44-45; 232pp; English.
XX
XX The invention relates to a peptide or polypeptide comprising an Fv
CC molecule, a construct or fragments or a construct of a fragment with
CC enhanced binding characteristics which selectively and/or specifically
CC binds to a target cell in favour of other cells, where binding is
CC primarily determined by a first hypervariable region and Fv is a single
CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
CC association with or attached, coupled, combined, linked or fused to a
CC pharmaceutical agent, is useful in the manufacture of a medicament, where
CC the medicament has activity against a diseased cell, preferably a cancer
CC cell (selected from carcinoma, sarcoma, leukemia, adenoma, lymphoma,
CC myeloma, blastoma, seminoma, and melanoma, where the leukemia cell is an
CC acute myeloid leukemia cell). The peptide is also useful for preparing a
CC composition for use in inhibiting the growth of a diseased or cancer
CC cell. This sequence represents a human Fv molecule hypervariable region
CC related peptide of the invention
XX
SQ Sequence 246 AA;

Query Match 100.0%; Score 29; DB 5; Length 246;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 6
| | | | |
| | | | |
Db 100 MRAPI 105

RESULT 7
ABG92026
ID ABG92026 standard; protein; 246 AA.
XX
AC ABG92026;

XX
DT 04-DEC-2002 (first entry)
XX
XX Antibody protein #5.
DE
XX
KW Antibody; epitope; cancer; tumour; cell rolling; inflammation;
KW metastasis; hypervariable region; autoimmune disease; thrombosis;
KW restenosis; leukemia; inflammatory disease; cardiovascular disease;
KW myocardial infarction; retinopathic disease; abnormal platelet function;
KW sulphated tyrosine-dependent protein-protein interaction.
XX
OS Unidentified.
XX
PN WO200253700-A2.
XX
PD 11-JUL-2002.
XX
PF 31-DEC-2001; 2001WO-US049442.
XX
PR 29-DEC-2000; 2000US-00751181.
PR 29-DEC-2000; 2000US-0258948P.
XX
PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX
PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
PI Szanton E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
DR WPI; 2002-674776/72.
XX
XX Novel isolated epitope present on cancer cells and important in
PT physiological phenomena such as cell rolling, metastasis and
PT inflammation, for treating autoimmune, inflammatory or cardiovascular
PT diseases, and cancer.
XX
PS Disclosure; Fig 52; 0pp; English.
XX
XX The invention relates to an isolated epitope present on cancer cells and
CC important in physiological phenomena such as cell rolling, metastasis and
CC inflammation, where the epitope is capable of being bound by an antibody,
CC its antigen-binding fragment or its complex comprising at least one
CC antibody or its binding fragment having a first hypervariable region. The
CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
CC tumour or leukemia cells, increase in number of tumour or leukemia
CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
CC platelet and/or cell-platelet adhesion or aggregation, for increasing
CC mortality of tumour or leukemia cells, for increasing the susceptibility
CC of diseased cells to damage by anti-disease, anti-cancer or anti-
CC leukemia agents, or for decreasing the number of tumour or leukemia
CC cells in a patient, or in the manufacture of a medicament for the above
CC mentioned purposes. The epitopes are useful for diagnosing and treating
CC diseases such as cancer, leukemia, autoimmune diseases, inflammatory
CC diseases, cardiovascular diseases such as myocardial infarction,
CC retinopathic diseases and other diseases mediated by abnormal platelet
CC function and diseases caused by sulphated tyrosine-dependent protein-
CC protein interactions. This sequence represents an antibody protein of the
CC invention
XX
SQ Sequence 246 AA;

Query Match 100.0%; Score 29; DB 5; Length 246;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 6
| | | | |
| | | | |
Db 100 MRAPI 105

RESULT 8
ABG78334
ID ABG78334 standard; protein; 256 AA.
XX

AC ABG78334;
 XX
 DT 15-NOV-2002 (first entry)
 XX
 DE Human Fv molecule hypervariable region related peptide #209.
 XX
 KM Human; Fv molecule; hypervariable region; single chain Fv; cyrostatic;
 KM disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukemia; adenoma;
 KM lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200259264-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 31-DEC-2001; 2001WO-US049440.
 XX
 PR 29-DEC-2000; 2000US-00751181.
 XX
 PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
 XX
 PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
 PI Plakain D, Peretz T;
 XX
 DR WPI; 2002-619166/66.
 XX
 PT Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
 PT or fragment, or construct of fragment with enhanced binding
 PT characteristics so as to selectively bind target cell in favor of other
 PT cells.
 XX
 PS Example 9; Page 90; 232pp; English.
 XX
 CC The invention relates to a peptide or polypeptide comprising an Fv
 CC molecule, a construct or fragments or a construct of a fragment with
 CC enhanced binding characteristics which selectively and/or specifically
 CC binds to a target cell in favour of other cells, where binding is
 CC primarily determined by a first hypervariable region and Fv is a single
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
 CC association with or attached, coupled, combined, linked or fused to a
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where
 CC the medicament has activity against a diseased cell, preferably a cancer
 CC cell (selected from carcinoma, sarcoma, leukemia, adenoma, lymphoma,
 CC myeloma, blastoma, seminoma, and melanoma, where the leukemia cell is an
 CC acute myeloid leukemia cell). The peptide is also useful for preparing a
 CC composition for use in inhibiting the growth of a diseased or cancer
 CC cell. This sequence represents a human Fv molecule hypervariable region
 CC related peptide of the invention
 CC
 SQ Sequence 256 AA;
 XX
 XX

Query Match 100.0%; Score 29; DB 5; Length 256;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
 |||||
 Db 100 MRAPVI 105

RESULT 9
 ABG92025 standard; protein; 256 AA.
 XX
 AC ABG92025;
 XX
 DT 04-DEC-2002 (first entry)
 XX
 DE Antibody biotag #1.
 XX
 KM Antibody; antibody biotag; cancer; tumour; cell rolling; inflammation;
 KM metastasis; hypervariable region; autoimmune disease; thrombosis;

KM restenosis; leukemia; inflammatory disease; cardiovascular disease;
 KM myocardial infarction; retinopathic disease; abnormal platelet function;
 KM sulphated tyrosine-dependent protein-protein interaction.
 XX
 OS Unidentified.
 XX
 PN WO200253700-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 31-DEC-2001; 2001WO-US049442.
 XX
 PR 29-DEC-2000; 2000US-00751181.
 XX
 PR 29-DEC-2000; 2000US-0258948P.
 XX
 PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
 XX
 PI Lazarovits J, Hagai Y, Plakain D, Vogel T, Nimrod A, Mar-Haim H;
 PI Szanton E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
 XX
 DR WPI; 2002-674776/72.
 XX
 PT Novel isolated epitope present on cancer cells and important in
 PT physiological phenomena such as cell rolling, metastasis and
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular
 PT diseases, and cancer.
 XX
 PS Disclosure; Fig 51; 0pp; English.
 XX
 CC The invention relates to an isolated epitope present on cancer cells and
 CC important in physiological phenomena such as cell rolling, metastasis and
 CC inflammation, where the epitope is capable of being bound by an antibody,
 CC its antigen-binding fragment or its complex comprising at least one
 CC antibody or its binding fragment having a first hypervariable region. The
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
 CC tumour or leukemia cells, increase in number of tumour or leukemia
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing
 CC mortality of tumour or leukemia cells, for increasing the susceptibility
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-
 CC leukemia agents, or for decreasing the number of tumour or leukemia
 CC cells in a patient, or in the manufacture of a medicament for the above
 CC mentioned purposes. The epitopes are useful for diagnosing and treating
 CC diseases such as cancer, leukemia, autoimmune diseases, inflammatory
 CC diseases, cardiovascular diseases such as myocardial infarction,
 CC retinopathic diseases and other diseases mediated by abnormal platelet
 CC function and diseases caused by sulphated tyrosine-dependent protein-
 CC protein interactions. This sequence represents an antibody biotag used in
 CC the scope of the invention
 CC
 SQ Sequence 256 AA;
 XX
 XX

Query Match 100.0%; Score 29; DB 5; Length 256;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
 |||||
 Db 100 MRAPVI 105

RESULT 10
 ABG92020 standard; protein; 266 AA.
 XX
 AC ABG92020;
 XX
 DT 04-DEC-2002 (first entry)
 XX
 DE Human antibody fragment #204.
 XX
 KM Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;

KW metastasis; hypervariable region; autoimmune disease; thrombosis;
KM restenosis; leukemia; inflammatory disease; cardiovascular disease;
KW myocardial infarction; retinopathic disease; abnormal platelet function;
KW sulphated tyrosine-dependent protein-protein interaction.
XX
OS Homo sapiens.
XX
PN WO200253700-A2.
XX
PD 11-JUL-2002.
XX
PF 31-DEC-2001; 2001WO-US049442.
XX
PR 29-DEC-2000; 2000US-00751181.
XX
PR 29-DEC-2000; 2000US-0258948P.
XX
PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX
PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
PI Szanton E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
XX
DR MPI; 2002-674776/72.
XX
PT Novel isolated epitope present on cancer cells and important in
PT physiological phenomena such as cell rolling, metastasis and
PT inflammation, for treating autoimmune, inflammatory or cardiovascular
PT diseases, and cancer.
XX
PS Disclosure, Page 309-310; Opp; English.
XX
CC The invention relates to an isolated epitope present on cancer cells and
CC important in physiological phenomena such as cell rolling, metastasis and
CC inflammation, where the epitope is capable of being bound by an antibody,
CC its antigen-binding fragment or its complex comprising at least one
CC antibody or its binding fragment having a first hypervariable region. The
CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
CC tumor or leukemia cells, increase in number of tumor or leukemia
CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
CC platelet and/or cell-platelet adhesion or aggregation, for increasing
CC mortality of tumor or leukemia cells, for increasing the susceptibility
CC of diseased cells to damage by anti-disease, anti-cancer or anti-
CC leukemia agents, or for decreasing the number of tumor or leukemia
CC cells in a patient, or in the manufacture of a medicament for the above
CC mentioned purposes. The epitopes are useful for diagnosing and treating
CC diseases such as cancer, leukemia, autoimmune diseases, inflammatory
CC diseases, cardiovascular diseases such as myocardial infarction,
CC retinopathic diseases and other diseases mediated by abnormal platelet
CC function and diseases caused by sulphated tyrosine-dependent protein-
CC protein interactions. This sequence represents a human antibody fragment
CC of the invention
CC
SQ Sequence 266 AA;
XX
Query Match 100.0%; Score 29; DB 5; Length 266;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRAPVI 6
DB 121 MRAPVI 126
XX
RESULT 11
ABG78150
ID ABG78150 standard; protein; 277 AA.
XX
AC ABG78150;
XX
KW Human Fv molecule hypervariable region related peptide #25.
XX
DT 15-NOV-2002 (first entry)
XX
DE Human Fv molecule hypervariable region related peptide #25.
XX

KW Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukemia; adenoma;
KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukemia.
XX
OS Homo sapiens.
XX
PN WO200259264-A2.
XX
PD 01-AUG-2002.
XX
PF 31-DEC-2001; 2001WO-US049440.
XX
PR 29-DEC-2000; 2000US-00751181.
XX
PR 29-DEC-2000; 2000US-00751181.
XX
PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX
PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
PI Plaksin D, Peretz T;
XX
DR MPI; 2002-619166/66.
XX
PT Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
PT or fragment, or construct of fragment with enhanced binding
PT characteristics so as to selectively bind target cell in favor of other
PT cells.
XX
PS Claim 4; Page 155-156; 232pp; English.
XX
CC The invention relates to a peptide or polypeptide comprising an Fv
CC molecule, a construct or fragments or a construct of a fragment with
CC enhanced binding characteristics which selectively and/or specifically
CC binds to a target cell in favour of other cells, where binding is
CC primarily determined by a first hypervariable region and Fv is a single
CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
CC association with or attached, coupled, combined, linked or fused to a
CC pharmaceutical agent, is useful in the manufacture of a medicament, where
CC the medicament has activity against a diseased cell, preferably a cancer
CC cell (selected from carcinoma, sarcoma, leukemia, adenoma, lymphoma,
CC myeloma, blastoma, seminoma, and melanoma, where the leukemia cell is an
CC acute myeloid leukemia cell). The peptide is also useful for preparing a
CC composition for use in inhibiting the growth of a diseased or cancer
CC cell. This sequence represents a human Fv molecule hypervariable region
CC related peptide of the invention
CC
SQ Sequence 277 AA;
XX
Query Match 100.0%; Score 29; DB 5; Length 277;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRAPVI 6
DB 121 MRAPVI 126
XX
RESULT 12
ABG91841
ID ABG91841 standard; protein; 277 AA.
XX
AC ABG91841;
XX
DT 04-DEC-2002 (first entry)
XX
DE Human antibody fragment #25.
XX
KW Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
KW metastasis; hypervariable region; autoimmune disease; thrombosis;
KW restenosis; leukemia; inflammatory disease; cardiovascular disease;
KW myocardial infarction; retinopathic disease; abnormal platelet function;
KW sulphated tyrosine-dependent protein-protein interaction.
XX
OS Homo sapiens.
XX

PN WO200253700-A2.
XX
PD 11-JUL-2002.
XX
XX 31-DEC-2001; 2001WO-US049442.
XX
XX 29-DEC-2000; 2000US-00751181.
PR 29-DEC-2000; 2000US-0258948P.
XX
XX (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX
PI Lazarevits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
PI Stanthon E, Richter T, Amit B, Kooperman L, Perez T, Levanon A;
XX
XX WPI; 2002-674776/72.
XX
XX Novel isolated epitope present on cancer cells and important in
PT physiological phenomena such as cell rolling, metastasis and
PT inflammation, for treating autoimmune, inflammatory or cardiovascular
PT diseases, and cancer.
XX
XX Claim 23; Page 233-234; Opp; English.
XX
XX The invention relates to an isolated epitope present on cancer cells and
CC important in physiological phenomena such as cell rolling, metastasis and
CC inflammation, where the epitope is capable of being bound by an antibody,
CC its antigen-binding fragment or its complex comprising at least one
CC antibody or its binding fragment having a first hypervariable region. The
CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
CC tumor or leukemia cells, increase in number of tumor or leukemia
CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
CC platelet and/or cell-platelet adhesion or aggregation, for increasing
CC mortality of tumor or leukemia cells, for increasing the susceptibility
CC of diseased cells to damage by anti-disease, anti-cancer or anti-
CC leukemia agents, or for decreasing the number of tumor or leukemia
CC cells in a patient, or in the manufacture of a medicament for the above
CC mentioned purposes. The epitopes are useful for diagnosing and treating
CC diseases such as cancer, leukemia, autoimmune diseases, inflammatory
CC diseases, cardiovascular diseases such as myocardial infarction,
CC retinopathic diseases and other diseases mediated by abnormal platelet
CC function and diseases caused by sulphated tyrosine-dependent protein-
CC protein interactions. This sequence represents a human antibody fragment
CC of the invention
XX
SQ Sequence 277 AA;
XX
XX Query Match 100.0%; Score 29; DB 5; Length 277;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRAPVI 6
DB 121 MRAPVI 126
XX
XX RESULT 13
AD128366
ID AD128366 standard; protein; 277 AA.
XX
XX AC AD128366;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE Human scFv fragment Y1, binds to platelets.
XX
XX KM Human; antibody; scFv; platelet; drug delivery; cancer; therapy.
OS Homo sapiens.
XX
XX PN WO2004002528-A1.
PD 08-JAN-2004.
XX

XX
XX 30-JUN-2003; 2003WO-US020604.
XX
XX PD 01-JUL-2002; 2002US-00189025.
XX
XX (SAVI-) SAVIENT PHARM INC.
XX
XX PI Lazarevits J, Nimrod A, Hoch-Mar-Chaim H, Levanon A;
XX
XX WPI; 2004-099189/10.
XX
XX Composition comprising an agent and/or antibody or its fragment, useful
PT for treating autoimmune disease, thrombosis, restenosis, metastasis, or
PT for inhibiting growth and/or replication of tumor cells or leukemia
PT cells.
XX
XX Claim 13; SEQ ID NO 1; 58pp; English.
XX
XX The present sequence is the protein sequence of human scFv fragment Y1.
CC This antibody was identified by screening a human antibody phage library
CC that has diversity only in the heavy chain CDR3 regions. Fixed human
CC platelets were screened in order to identify antibodies that bind
CC platelets. The epitope for Y1 antibody is located between amino acids 272
CC and 285 on glycocalicin, a subunit of the CD42 complex. Y1 also binds the
CC N-terminal of PSGL-1, a receptor for E-, L- and P-selectins, and has a
CC high affinity for primary leukemia cells. The invention relates to
CC compositions utilising an agent and an antibody or its fragment. The
CC agent is a toxin, radioisotope or pharmaceutical agent such as
CC doxorubicin. It is complexed or combined with or conjugated to the
CC antibody or its fragment. The agent and/or antibody can be present in the
CC composition is a sub-clinical amount, i.e. less than the amount generally
CC found to be clinically effective when the agent is administered alone.
CC The composition is used in claimed methods of: inhibiting cell rolling,
CC inflammation, thrombosis, restenosis, metastasis, the growth and/or
CC replication of tumor cells or leukemia cells, an increase in number of
CC tumor or leukemia cells, cell-cell, cell-matrix, platelet-matrix,
CC platelet-platelet and/or cell-platelet complex formation, aggregation or
CC adhesion; increasing the mortality rate of tumor or leukemia cells, the
CC susceptibility of disease cells to damage by anti-disease agents, and the
CC susceptibility of tumor or leukemia cells to damage by anti-cancer
CC agents; and ameliorating the effects of a disease, preventing a disease,
CC treating a disease or inhibiting the progress of a disease.
XX
SQ Sequence 277 AA;
XX
XX Query Match 100.0%; Score 29; DB 8; Length 277;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRAPVI 6
DB 121 MRAPVI 126
XX
XX RESULT 14
AD128367
ID AD128367 standard; protein; 278 AA.
XX
XX AC AD128367;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE Human scFv fragment Y17, binds to platelets.
XX
XX KM Human; antibody; scFv; platelet; drug delivery; cancer; therapy.
OS Homo sapiens.
XX
XX PN WO2004002528-A1.
PD 08-JAN-2004.
XX
XX PF 30-JUN-2003; 2003WO-US020604.
XX

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OM protein - protein search, using sw model

Run on: September 9, 2005, 16:13:21 ; Search time 17.7 Seconds
(Without alignments)
32.616 Million cell updates/sec

Title: US-10-032-037C-8

Perfect score: 29

Sequence: 1 MRAPI 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.79:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	249	2 H87675	hydroxylase, alpha/b
2	29	100.0	442	2 JC4733	probable H+-transp
3	29	100.0	629	2 T37255	acetylcholinesterase
4	28	96.6	425	2 S33045	hypothetical prote
5	27	93.1	247	2 H69030	coenzyme PQQ synth
6	26	89.7	286	2 A91131	tagatose-1,6-bisph
7	26	89.7	286	2 A85976	tagatose-bisphosph
8	26	89.7	286	2 E65103	tagatose-bisphosph
9	26	89.7	327	2 E72057	ferrochelatase CP0
10	26	89.7	327	2 H85655	ferrochelatase [im
11	26	89.7	450	1 S13730	pmba protein - Bsc
12	26	89.7	450	2 A81056	probable pmba prot
13	26	89.7	450	2 D86121	maturatation of anti
14	26	89.7	450	2 D91280	maturatation of anti
15	26	86.2	138	2 T24916	hypothetical prote
16	25	86.2	147	2 C95907	hypothetical prote
17	25	86.2	147	2 P95924	hypothetical prote
18	25	86.2	149	2 C72419	conserved hypochet
19	25	86.2	154	2 A82812	conserved hypochet
20	25	86.2	163	2 A87412	hypothetical prote
21	25	86.2	195	2 F75399	antibiotic resista
22	25	86.2	196	2 G75405	probable amidoran
23	25	86.2	203	2 C84409	imidazoleglycerol-
24	25	86.2	222	2 S63320	probable membrane
25	25	86.2	222	2 S56195	probable membrane
26	25	86.2	224	2 S55081	hypothetical prote
27	25	86.2	227	2 C53304	transfer protein C
28	25	86.2	240	2 E69004	hypothetical prote
29	25	86.2	252	2 A88508	protein H14A12.4 [

30	25	86.2	261	2 AC3507	hisf protein [impo
31	25	86.2	266	2 AC2407	tryptophan synthas
32	25	86.2	284	2 AF1341	fructose-1,6-bispho
33	25	86.2	284	2 AD1712	fructose-1,6-bispho
34	25	86.2	328	2 G96024	conserved hypochet
35	25	86.2	332	2 C81285	glyceraldehyde 3-P
36	25	86.2	359	2 A10112	fructose-bisphosph
37	25	86.2	352	2 P90200	hypothetical prote
38	25	86.2	398	2 B70752	hypothetical prote
39	25	86.2	422	2 AE3394	lipoprotein releas
40	25	86.2	422	2 E83083	probable two-compo
41	25	86.2	430	2 T16715	hypothetical prote
42	25	86.2	446	2 A84940	pmba protein [impo
43	25	86.2	463	2 AC0977	L-seryl-tRNAse
44	25	86.2	487	2 T27353	hypothetical prote
45	25	86.2	489	2 JC4787	shaw protein - Cal

ALIGNMENTS

RESULT 1
H87675 hydroxylase, alpha/beta hydroxylase fold family [imported] - Caulobacter crescentus
C/Species: Caulobacter crescentus
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #ext_change 12-Jul-2004
C/Accession: H87675
R/Merman, W.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gilm, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A/Title: Complete Genome Sequence of Caulobacter crescentus.
A/Reference number: AB7249; UID:21173698; PMID:11259647
A/Accession: H87675
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1249 <STO>
A/Cross-references: UNIPROT:Q9A2M4; GB:AE005673; NID:G13425158; PIDN:AAK25404.1; GSPDB:
C/Genetics:
A/Gene: CC3442
C/Superfamily: tropinesterase

Query Match 100.0%; Score 29; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPI 6
Db 1 MRAPI 6

RESULT 2
JC4733 hydroxylase, alpha/beta hydroxylase fold family [imported] - Rhodospirillum rubrum
C/Species: Rhodospirillum rubrum
C/Date: 10-May-1996 #sequence_revision 19-Jul-1996 #ext_change 09-Jul-2004
C/Accession: JC4733
R/Ballado, T.; Campos, A.; Camarena, L.; Dreyfus, G.
Gene 170, 69-72, 1996
A/Title: Flagellar genes from Rhodospirillum rubrum are homologous to genes of the fl
A/Reference number: JC4733; UID:96200857; PMID:8621091
A/Accession: JC4733
A/Molecule type: DNA
A/Residues: 1442 <BAL>
A/Cross-references: UNIPROT:Q53093; GB:U31090; NID:G1518877; PIDN:AA807344.1; PID:G129325

A/Gene: flII
C/Superfamily: H+-transporting ATP synthase alpha chain; H+-transporting ATP synthase al
C/Keywords: ATP; flagellum; hydroxylase; nucleotide binding; P-loop
F:168-175/Region: nucleotide-binding motif A (P-loop)
F:191-362/Region: H+-transporting ATP synthase alpha chain homology <ATP>
F:191-207/Region: ATP-binding #status predicted
F:242-258/Domain: beta chain #status predicted <BET>

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Query Match          100.0%; Score 29; DB 2; Length 442;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
Db 77 MRAPVI 82

RESULT 3
T37255
acetylcholinesterase (EC 3.1.1.7) 2 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: T37255
R/Guano, M.; Culetto, E.; Combes, D.; Fedon, Y.; Toutant, J.P.; Arpagaus, M.
FEBS Lett. 424, 279-284, 1998
A/Title: Existence of four acetylcholinesterase genes in the nematode Caenorhabditis el
A/Reference number: Z21648; MUID:98198570; PMID:9539167
A/Accession: T37255
A/Status: preliminary; translated from GB/EMBL/DBD
A/Molecule type: mRNA
A/Residues: 1-629 <GRA>
A/Cross-references: UNIPROT:O61371; EMBL:AF025378; NID:G5148937; PIDN:AA14016.2; PID:G5
A/Experimental source: strain N2
C/Genetics:
A/Map position: I
C/Superfamily: cholinesterase; cholinesterase homology
C/Keywords: carboxylic ester hydrolase

Query Match          100.0%; Score 29; DB 2; Length 629;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
Db 1 MRAPVI 6

RESULT 4
S33045
hypothetical protein - human herpesvirus 4
C/Species: human herpesvirus 4, Epstein-Barr virus
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S33045
R/Fairall, P.O.
submitted to the EMBL Data Library, March 1988
A/Reference number: S32973
A/Accession: S33045
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-425 <PAR>
A/Cross-references: UNIPROT:P30119; EMBL:V01555; NID:G59074; PIDN:CAA24796.1; PID:G13349
C/Superfamily: equine herpesvirus 2 hypothetical protein 23

Query Match          96.6%; Score 28; DB 2; Length 425;
Best Local Similarity 83.3%; Pred. No. 42;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
Db 87 MRAPVI 92

RESULT 5
H69030
coenzyme PQQ synthesis protein III - Methanobacterium thermoautotrophicum (strain Delta
C/Species: Methanobacterium thermoautotrophicum
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C/Accession: H69030
R/Smith, D.R.; Doucet-Stamm, L.A.; Delouhery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
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; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J Bacteriol. 179, 7135-7155, 1997
A/Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A/Reference number: A69000; MUID:98037514; PMID:9371463
A/Accession: H69030
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-247 <MTH>
A/Cross-references: UNIPROT:Q27295; GB:AE000890; GB:AE000666; NID:G2622331; PIDN:AA8571
A/Experimental source: strain Delta H
C/Genetics:
A/Gene: MTH1227
A/Start codon: GTG
C/Keywords: iron; metalloprotein
F,34,38,41/Binding site: iron (Cys) #status predicted

Query Match          93.1%; Score 27; DB 2; Length 247;
Best Local Similarity 66.7%; Pred. No. 42;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
Db 4 MRAPVI 9

RESULT 6
A91131
tagatose-1,6-bisphosphate aldolase [imported] - Escherichia coli (strain O157:H7, substra
C/Species: Escherichia coli
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C/Accession: A91131
R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A/Reference number: A99629; MUID:21156231; PMID:11258796
A/Accession: A91131
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-286 <HAY>
A/Cross-references: UNIPROT:P42908; GB:BA000007; PIDN:BA837440.1; PID:G13363490; GSPDB:G
A/Experimental source: strain O157:H7, substrain RIMD 0509952
C/Genetics:
A/Gene: BCG4017
C/Superfamily: fructose-bisphosphate aldolase II

Query Match          89.7%; Score 26; DB 2; Length 286;
Best Local Similarity 83.3%; Pred. No. 89;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
Db 41 MRAPVI 46

RESULT 7
A85976
tagatose-bisphosphate aldolase 2 [imported] - Escherichia coli (strain O157:H7, substra
C/Species: Escherichia coli
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C/Accession: A85976
R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Diallanza, E.; Potamouets, K.; Apodaca,
Nature 409, 529-533, 2001
A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A/Reference number: A85480; MUID:21074935; PMID:11206551
A/Accession: A85976
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-286 <STO>
A/Cross-references: UNIPROT:P42908; GB:AE005174; NID:G12517735; PIDN:AA658269.1; GSPDB:G
A/Experimental source: strain O157:H7, substrain EDL933
```

C/Genetics:
A/Gene: agay
C/Superfamily: fructose-bisphosphate aldolase II

Query Match 89.7%; Score 26; DB 2; Length 286;
Best Local Similarity 83.3%; Pred. No. 89;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
|||
41 MRSPVI 46

RESULT 8

ferrochelatase CP0144 [imported] - Chlamydia pneumoniae (strain K-12)
C/Species: Escherichia coli
C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004

C/Accession: B65103
R/Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997

A/Title: The complete genome sequence of Escherichia coli K-12.

A/Reference number: A64720; MUID:97426617; PMID:9278503

A/Accession: B65103

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-286 <BLAT>

A/Cross-references: UNIPROT:P42908; GB:AE000395; GB:U00096; NID:g1789524; PIDN:AACT6171.

A/Experimental source: strain K-12, substrain MG1655

C/Genetics:

A/Gene: agay

C/Superfamily: fructose-bisphosphate aldolase II

C/Keywords: aldehyde-lyase; carbon-carbon lyase

Query Match 89.7%; Score 26; DB 2; Length 286;
Best Local Similarity 83.3%; Pred. No. 89;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
|||
41 MRSPVI 46

RESULT 9

ferrochelatase CP0144 [imported] - Chlamydia pneumoniae (strains CWL029 and AR39)
C/Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C/Accession: E72057; F81609

R/Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.

Nature Genet. 21, 385-389, 1999

A/Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.

A/Reference number: A72000; MUID:99206606; PMID:10192388

A/Accession: E72057

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-327 <AN>

A/Cross-references: UNIPROT:Q9Z7V1; GB:AE001645; GB:AE001363; NID:g4376896; PIDN:AAD1874

A/Experimental source: strain CWL029

R/Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,

C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,

Nucleic Acids Res. 28, 1397-1406, 2000

A/Title: Genome sequences of Chlamydia trachomatis Mogen and Chlamydia pneumoniae AR39.

A/Reference number: AB1500; MUID:20150255; PMID:10684935

A/Accession: F81609

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-327 <RNA>

A/Cross-references: GB:AE002175; GB:AE002161; NID:g7189069; PIDN:AAF38026.1; PID:g718907

A/Experimental source: strain AR39, HL cells

C/Genetics:

A/Gene: hemZ, CP0144

C/Superfamily: ferrochelatase

Query Match 89.7%; Score 26; DB 2; Length 327;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
|||
86 MRAPVI 91

RESULT 10

ferrochelatase [imported] - Chlamydia pneumoniae (strain J138)
H86565
C/Species: Chlamydia pneumoniae, Chlamydia pneumoniae

C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C/Accession: H86565

R/Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishii, F.; Ouchi, K.; Shiba, T.; I-

Nucleic Acids Res. 28, 2311-2314, 2000

A/Title: Comparison of whole genome sequences of Chlamydia pneumoniae J138.

A/Reference number: A86491; MUID:20330349; PMID:10871362

A/Accession: H86565

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-327 <STO>

A/Cross-references: UNIPROT:Q9Z7V1; GB:BA000008; NID:g8978975; PIDN:BA98810.1; GSPDB:GN

A/Experimental source: strain J138

C/Genetics:

A/Gene: hemZ

Query Match 89.7%; Score 26; DB 2; Length 327;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
|||
86 MRAPVI 91

RESULT 11

pmbA protein - Escherichia coli (strain K-12)
S13730

C/Species: Escherichia coli

C/Date: 29-Jan-1999 #sequence_revision 29-Jan-1999 #text_change 09-Jul-2004

C/Accession: S13730; S56461; F65235

R/Rodriguez-Sainz, M.C.; Hernandez-Chico, C.; Moreno, F.

Mol. Microbiol. 4, 1921-1932, 1990

A/Title: Molecular characterization of pmbA, an Escherichia coli chromosomal gene reguli.

A/Reference number: S13730; MUID:91186828; PMID:2082149

A/Accession: S13730

A/Molecule type: DNA

A/Residues: 1-450 <RNA>

A/Cross-references: UNIPROT:P24231; EMBL:X54152; NID:g42439; PIDN:CAA38091.1; PID:g42440

R/Burland, V.; Plunkett III, G.; Sofia, H.T.; Daniels, D.L.; Blattner, F.R.

Nucleic Acids Res. 23, 2105-2119, 1995

A/Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92

A/Reference number: S56314; MUID:95334362; PMID:7610040

A/Accession: S56461

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-450 <RNA>

A/Cross-references: EMBL:U14003; NID:g1263172; PIDN:AA97132.1; PID:g537077

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994

R/Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A/Title: The complete genome sequence of Escherichia coli K-12.

A/Reference number: A64720; MUID:97426617; PMID:9278503

A/Accession: F65235

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-450 <BLAT>

A/Cross-references: GB:AE000494; GB:U00096; NID:g1790670; PIDN:AACT7192.1; PID:g1790682,

A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: pmdb
A:Map position: 96 min
C:Superfamily: Escherichia coli pmdb protein

Query Match 89.7%; Score 26; DB 1; Length 450;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPIV 6
DB 242 MKAPVI 247

RESULT 12
AE1056

probable pmdb protein pmdb [imported] - Salmonella enterica subsp. enterica serovar Typh
C:Species: Salmonella enterica subsp. enterica serovar Typh
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AE1056

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, K.M.; Dowd, L.; White, N.; Farrar, S.; Moul, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skellton, J.; Stevens, K.; A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AE1056

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-450 <PAR>
A:Cross-references: GB:U153382; PIDN:CAD06898.1; PID:g16505546; GSPDB:GN00176
C:Genetics:

A:Gene: pmdb
C:Superfamily: Escherichia coli pmdb protein

Query Match 89.7%; Score 26; DB 2; Length 450;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPIV 6
DB 242 MKAPVI 247

RESULT 13
D86121

maturation of antibiotic MccB17, see tld genes [imported] - Escherichia coli (strain O15
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: D86121

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Illier, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: AB5480; MUID:21074935; PMID:11206551

A:Accession: D86121
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-450 <STO>
A:Cross-references: UNIPROT:P24231; GB:AB005174; NID:g12519236; PIDN:AAG59432.1; GSPDB:G
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: pmdb
C:Superfamily: Escherichia coli pmdb protein

Query Match 89.7%; Score 26; DB 2; Length 450;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPIV 6

DB 242 MKAPVI 247

RESULT 14
D91280

maturation of antibiotic MccB17 [imported] - Escherichia coli (strain O157:H7, substrain
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: D91280

R:Hayashi, T.; Makino, K.; Onishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kohara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: D91280
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-450 <HAY>
A:Cross-references: UNIPROT:P24231; GB:BA000007; PIDN:BA03635.1; PID:g13364689; GSPDB:G
C:Genetics:
A:Experimental source: strain O157:H7, substrain RIMD 0509952

A:Gene: EC65212
C:Superfamily: Escherichia coli pmdb protein

Query Match 89.7%; Score 26; DB 2; Length 450;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPIV 6
DB 242 MKAPVI 247

RESULT 15
T24916

hypothetical protein T14G10.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T24916

R:Wild, A.
submitted to the EMBL Data Library, January 1996
A:Reference number: T24916
A:Accession: T24916
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-138 <WIL>
A:Cross-references: UNIPROT:Q22499, EMBL:Z68880, PIDN:CAA93096.1, GSPDB:GN00022; CESP:TL
A:Experimental source: clone T14G10
C:Genetics:
A:Gene: CESP:T14G10.4
A:Map position: 4
A:introns: 52/3; 108/2

Query Match 86.2%; Score 25; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPIV 5
DB 1 MRAPIV 5

Search completed: September 9, 2005, 16:31:43
Job time : 19.7 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 9, 2005, 15:58:05 ; Search time 85.8 Seconds

(Without alignments)
35.810 Million cell updates/sec

Title: US-10-032-037C-8

Sequence: 1 MRAPV1 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: UniProt 03:*
1: uniprot_sprot:*
2: uniprot_tramb1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	249	09A2W4	09A2W4 caulobacter
2	29	100.0	309	063ZV1	063ZV1 mus musculus
3	29	100.0	442	053093	053093 rhodobacter
4	29	100.0	442	053153	053153 rhodobacter
5	29	100.0	629	061371	061371 caenorhabditis
6	29	100.0	939	06PD31	06PD31 mus musculus
7	29	100.0	947	080RL6	080RL6 mus musculus
8	28	96.6	164	1 RHBI_RAT	088779 ratius norv
9	28	96.6	231	1 Q6FD44	061d44 acinetobact
10	28	96.6	373	1 RHBI_MOUSE	08vcd2 mus musculu
11	28	96.6	376	1 Q8P9F5	08P9F5 xanthomonas
12	28	96.6	425	1 YTRL_EBV	030119 Epstein-bar
13	28	96.6	425	1 Q777C1	0777C1 human herpe
14	28	96.6	438	1 RHBI_HUMAN	075783 homo sapien
15	28	96.6	541	1 Q8NT69	08nt69 Corynebacte
16	28	96.6	577	1 Q6CYG3	06cyg3 kluveromyc
17	28	96.6	713	1 Q7YYX3	07yyx3 cryptospori
18	27	93.1	247	2 Q27295	027295 methanobact
19	27	93.1	376	2 Q9L778	09L778 xanthomonas
20	27	93.1	376	2 Q8P469	08P469 xanthomonas
21	27	93.1	416	2 Q9AC09	09acq9 streptomyce
22	27	93.1	449	2 Q89X81	089x81 bradyrhizob
23	27	93.1	535	1 TLK1_BRARE	013168 brachydanio
24	27	93.1	771	2 Q98TH2	098th2 brachydanio
25	26	89.7	162	2 Q8L1B7	08l1b7 plasmodium
26	26	89.7	199	2 Q7RLI3	07rl13 plasmodium
27	26	89.7	250	1 PDXJ_BRAJA	06bse3 debaryomyce
28	26	89.7	250	1 PDXJ_BRAJA	06bse3 debaryomyce
29	26	89.7	286	1 AGAY_BOOLI	07f2a7 cryza sacti
30	26	89.7	286	1 AGAY_BOOLI	07f2a7 cryza sacti
31	26	89.7	286	2 Q9KIF8	09kif8 escherichia

32	26	89.7	305	2 Q65WZ6	065wz6 bacillus 11
33	26	89.7	327	1 HEMZ_CHLPP	09z7v1 chlamydia p
34	26	89.7	353	2 Q9TE68	09te68 nitzschia f
35	26	89.7	353	2 Q9TE71	09te71 cylindrothe
36	26	89.7	450	1 PMBA_ECOLI	P24231 escherichia
37	26	89.7	450	2 Q8XGJ7	08xgj7 salmonella
38	26	89.7	450	2 Q7CP84	07cp84 salmonella
39	26	89.7	450	2 Q7UDN7	07udn7 shigella fl
40	26	89.7	450	2 Q83P54	083p54 shigella fl
41	26	89.7	450	2 Q8FAF2	08faf2 escherichia
42	26	89.7	463	2 Q7UKY8	07uky8 rhodospirill
43	26	89.7	535	2 Q8BER8	08ber8 oceanobacti
44	26	89.7	583	2 Q9VKE5	09vke5 dirosophila
45	26	89.7	1042	2 Q7QXR0	07qxr0 giardia lam

ALIGNMENTS

RESULT 1	ID	Score	DB 2	Length	249
09A2W4	PRELIMINARY;	PRT;	249	AA.	
AC	09A2W4				
DT	01-JUN-2001 (T-EMBLrel. 17, Created)				
DT	01-JUN-2001 (T-EMBLrel. 17, Last sequence update)				
DT	01-MAR-2004 (T-EMBLrel. 26, Last annotation update)				
DE	Hydrolyase, alpha/beta hydrolyase fold family.				
GN	OrderedlocusNames=CC3442;				
OS	Caulobacter crescentus.				
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;				
OC	Caulobacteraceae; Caulobacter.				
OX	NCBI_Taxid=155892;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=ATCC 19089 / CB15;				
RX	MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;				
RA	Nierman W.C., Feldblyum T.V., Taub M.T., Paulsen I.T., Nelson K.E.,				
RA	Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,				
RA	DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,				
RA	Kolony J.F., Smit J., Craven M.B., Kouri H.M., Shetty J.,				
RA	Berry K.J., Uterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,				
RA	Emmolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,				
RA	Frazer C.M.;				
RT	"Complete genome sequence of Caulobacter crescentus.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141 (2001).				
DR	EMBL; AB006003; AAK25404.1; -				
DR	PIR; H87675; H87675.				
DR	TIGR; CC3442; -				
DR	GO; GO:0016787; F:hydrolyase activity; IEA.				
DR	GO; GO:0006725; P:aromatic compound metabolism; IEA.				
DR	InterPro; IPR000073; A/b hydrolyase.				
DR	InterPro; IPR003089; AB hydrolyase.				
DR	InterPro; IPR000379; Set_sacres.				
DR	Pfam; PF00561; Abhydrolyase_1; 1.				
DR	PRINTS; PR00111; ABHYDROLASE.				
KW	Complete proteome; Hydrolyase.				
SQ	SEQUENCE 249 AA; 26772 MW; 491350127DD300AE CRC64;				
Query Match	100.0%;	Score 29;	DB 2;	Length 249;	
Best Local Similarity	100.0%;	Pred. No. 65;			
Matches 6;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1 MRAPV1 6				
DB	1 MRAPV1 6				
RESULT 2					
ID	063ZV1	PRELIMINARY;	PRT;	309	AA.
AC	063ZV1				
DT	25-OCT-2004 (T-EMBLrel. 28, Created)				

DT 25-OCT-2004 (TrEMBLrel. 28, last sequence update)
 DE Hypothetical protein (Fragment).
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Mouse;
 RX PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Krausberg R.L., Feingold E.A., Groise L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.L., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uebachs T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fehy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skaleka U., Smallus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Mouse;
 RA Director MGC Project;
 RA Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC082807; AA82807.1; -.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 309 AA; 32959 MW; 5F551A9E90CC8714 CRC64;
 Query Match 100.0%; Score 29; DB 2; Length 309;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRAPVI 6
 DB 286 MRAPVI 291
 RESULT 3
 Q53093 PRELIMINARY; PRT; 442 AA.
 AC Q53093;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Fli1.
 GN Name=fli1;
 OS Rhodospirillum rubrum (Rhodospirillum rubrum).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
 OC Rhodospirillaceae; Rhodospirillum.
 NCBI_TaxID=1063;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=2.4.1;
 RX MEDLINE=96200857; PubMed=8621091; DOI=10.1016/0378-1119(95)00855-1;
 RA Ballado T., Campos A., Camarena L., Dreyfus G.;
 RT "Flaellar genes from Rhodospirillum rubrum are homologous to genes
 RT of the fli operon of Salmonella typhimurium and to the type-III
 RT secretion system.";
 RL Gene 170:69-72(1996).
 CC -1- SIMILARITY: Belongs to the ATPase alpha/beta chains family.

DR EMBL; U31090; AA807344.1; -.
 DR PIR; J4733; J4733.
 DR HSP; P03002; LPVO.
 DR GO; GO:0005737; Cytoplasm; IEA.
 DR GO; GO:0014634; Cytochrome-transporting two-sector ATPase complex; IEA.
 DR GO; GO:0005524; F1-ATP binding; IEA.
 DR GO; GO:0016887; F1-ATPase activity; IEA.
 DR GO; GO:0046933; F1-hydrogen-transporting ATP synthase activity; IEA.
 DR GO; GO:0046961; F1-hydrogen-transporting ATPase activity; IEA.
 DR GO; GO:0016787; F1-hydrogen-transporting ATPase activity; IEA.
 DR GO; GO:0000166; F1-ATPase activity; IEA.
 DR GO; GO:0015986; F1-ATP synthase coupled proton transport; IEA.
 DR GO; GO:0009058; P1-ATP synthase; IEA.
 DR GO; GO:0015031; P1-ATP synthase; IEA.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR000194; ATPase_a/b_centre.
 DR InterPro; IPR004100; ATPase_a/b_N.
 DR InterPro; IPR005714; F111_YscN.
 DR Pfam; PF00006; ATP-synt_ab; 1.
 DR SMART; SM00382; AAA; 1.
 DR TIGRfam; TIGR01026; fli1_YscN; 1.
 DR PROSITE; PS00152; ATPase_ALPHA_BETA; UNKNOWN_1.
 KW ATP synthesis; ATP-binding; Hydrolyase; Ion transport; Transport.
 SQ SEQUENCE 442 AA; 46852 MW; E6D3551F5A59BAE CRC64;
 Query Match 100.0%; Score 29; DB 2; Length 442;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRAPVI 6
 DB 77 MRAPVI 82
 RESULT 4
 Q53153 PRELIMINARY; PRT; 442 AA.
 AC Q53153;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Fli1 protein.
 GN Name=fli1;
 OS Rhodospirillum rubrum (Rhodospirillum rubrum).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
 OC Rhodospirillaceae; Rhodospirillum.
 NCBI_TaxID=1063;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WS8;
 RX MEDLINE=96327148; PubMed=8759796; DOI=10.1016/0378-1097(96)00252-2;
 RA Goodfellow I.G., Pollitt C.E., Sockete R.E.;
 RT "Cloning of the fli1 gene from Rhodospirillum rubrum by analysis
 RT of a transposon mutant with impaired motility.";
 RL FEMS Microbiol. Lett. 142:111-116(1996).
 CC -1- SIMILARITY: Belongs to the ATPase alpha/beta chains family.
 DR EMBL; X97201; CA65834.1; -.
 DR HSP; P03002; LPVO.
 DR GO; GO:0005737; Cytoplasm; IEA.
 DR GO; GO:0014634; Cytochrome-transporting two-sector ATPase complex; IEA.
 DR GO; GO:0005524; F1-ATP binding; IEA.
 DR GO; GO:0016887; F1-ATPase activity; IEA.
 DR GO; GO:0046933; F1-hydrogen-transporting ATP synthase activity; IEA.
 DR GO; GO:0046961; F1-hydrogen-transporting ATPase activity; IEA.
 DR GO; GO:0016787; F1-hydrogen-transporting ATPase activity; IEA.
 DR GO; GO:0000166; F1-ATPase activity; IEA.
 DR GO; GO:0015986; F1-ATP synthase coupled proton transport; IEA.
 DR GO; GO:0009058; P1-ATP synthase; IEA.
 DR GO; GO:0015031; P1-ATP synthase; IEA.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR000194; ATPase_a/b_centre.
 DR InterPro; IPR004100; ATPase_a/b_N.
 DR InterPro; IPR005714; F111_YscN.
 DR Pfam; PF00006; ATP-synt_ab; 1.
 DR SMART; SM00382; AAA; 1.
 DR TIGRfam; TIGR01026; fli1_YscN; 1.
 DR PROSITE; PS00152; ATPase_ALPHA_BETA; UNKNOWN_1.
 KW ATP synthesis; ATP-binding; Hydrolyase; Ion transport; Transport.
 SQ SEQUENCE 442 AA; 46852 MW; E6D3551F5A59BAE CRC64;

RA Barrett B.G.;
 RT "DNA sequence analysis of the EcoRI DheI fragment of B95-8 Epstein-
 RT Barr virus containing the terminal repeat sequences.";
 RL Mol. Biol. Med. 1:425-445 (1983).
 RN [11]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B95-8;
 RX MEDLINE=2033131; PubMed=10872327;
 RA Farrell P.J., Bankier A., Seguin C., Deininger P., Barrett B.G.;
 RT "Latent and -lytic cycle promoters of Epstein-Barr virus.";
 RL EMBO J. 2:1331-1338 (1983).
 RN [12]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B95-8;
 RX MEDLINE=84207939; PubMed=6327220;
 RA Jones M.D., Foster L., Sheehy T., Griffin B.B.;
 RT "The EB virus genome in Daudi Burkitt's lymphoma cells has a deletion
 RT similar to that observed in a non-transforming strain (P3HR-1) of the
 RT virus.";
 RL EMBO J. 3:813-821 (1984).
 RN [13]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B95-8;
 RX MEDLINE=84236104; PubMed=6203743;
 RA Biggin M., Farrell P.J., Barrett B.G.;
 RT "Transcription and DNA sequence of the BamHI L fragment of B95-8
 RT Epstein-Barr virus.";
 RL EMBO J. 3:1083-1090 (1984).
 RN [14]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B95-8;
 RX MEDLINE=84222045; PubMed=6328526;
 RA Yates J., Warren N., Reisman D., Sugden B.;
 RT "A cis-acting element from the Epstein-Barr viral genome that permits
 RT stable replication of recombinant plasmids in latently infected
 RT cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3806-3810 (1984).
 RN [15]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B95-8;
 RX MEDLINE=84247360; PubMed=6330697;
 RA Gibson T., Stockwell P., Ginsburg M., Barrett B.;
 RT "Homology between two EBV early genes and HSV ribonucleotide reductase
 RT and 38k genes.";
 RL Nucleic Acids Res. 12:5087-5099 (1984).
 RN [16]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B95-8;
 RX MEDLINE=87289053; PubMed=3039467;
 RA Bodescot M., Pericautaud M.;
 RT "Clustered alternative splice sites in Epstein-Barr virus RNAs.";
 RL Nucleic Acids Res. 15:5887-5897 (1987).
 RN [17]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B95-8;
 RX MEDLINE=91021036; PubMed=2171209;
 RA Parker B.D., Bankier A., Satchwell S., Barrett B., Farrell P.J.;
 RT "Sequence and transcription of Raji Epstein-Barr virus DNA spanning
 RT the B95-8 deletion region.";
 RL Virology 179:339-346 (1990).
 RN [18]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B95-8;
 RX MEDLINE=895-8;
 RA Hatfull G.F., Barrett B.G., Quinn J., McGeoch D.;
 RT Submitted (Oct-2002) to the EMBL/GenBank/DBD databases.
 RN [19]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B95-8;
 RX MEDLINE=895-8;
 RA Bime U.K., Amou W., Farrell P.J.;
 RT "Induction of Epstein-Barr virus late promoters on small plasmids in
 RT the EBV late lytic cycle requires ori lyt.";
 RL Submitted (Aug-2002) to the EMBL/GenBank/DBD databases.
 DR EMBL, AJ507799; CAD53449.1; -.

DR InterPro; IPR006772; Herpes_BTRFL.
 DR Pfam; PF04682; Herpes_BTRFL; 1.
 FT NON TER 1
 FT NON TER 425
 SO SEQUENCE 425 AA; 46711 MW; 0ECBCE5FD30495BD CRC64;
 Query Match 96.6%; Score 28; DB 2; Length 425;
 Best Local Similarity 83.3%; Pred. No. 2.1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRAPV 6
 Db 87 MRAPV 92
 RESULT 14
 ID RHBI_HUMAN STANDARD; PRT; 438 AA.
 AC 075783; OSNQ85;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Rhomboid-related protein 1 (EC 3.4.21.-) (RRP) (Rhomboid-like protein
 DE 1).
 GN Name=RHBDL1; Synonyms=RHBDL;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Leukemia;
 RX MEDLINE=98324821; PubMed=9662444; DOI=10.1016/S0014-5793(98)00622-X;
 RA Pascall J.C., Brown K.D.;
 RT "Characterization of a mammalian cDNA encoding a protein with high
 RT sequence similarity to the Drosophila regulatory protein Rhomboid.";
 RL FEBS Lett. 429:337-340 (1998).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=21096910; PubMed=1157797; DOI=10.1093/hmg/10.4.339;
 RA Daniels R.J., Peden J.F., Lloyd C., Horeley S.W., Clark K.,
 RA Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
 RA Higgins D.R.;
 RT "Sequence, structure and pathology of the fully annotated terminal 2
 RT Mb of the short arm of human chromosome 16.";
 RL Hum. Mol. Genet. 10:339-352 (2001).
 CC -1- FUNCTION: May be involved in regulated intramembrane proteolysis
 CC and the subsequent release of functional polypeptides from their
 CC membrane anchors (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=O75783-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=O75783-2; Sequence=VSP_005372;
 CC -1- TISSUE SPECIFICITY: Detected in heart, brain, skeletal muscle and
 CC kidney.
 CC -1- SIMILARITY: Belongs to the peptidase S54 family.
 CC -----
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 CC -----
 CC EMBL, Y17108; CAA76629.1; -.
 CC EMBL, AJ272344; CAC00640.1; -.
 CC EMBL, AE006464; AAK61241.1; -.
 CC MEROPS; S54.005; -.
 DR Genew; HGNC:10007; RHBDL1.

DR MIM; 603264; -.
 DR GO; GO:0005887; C:integral to plasma membrane; TMS.
 DR GO; GO:0005624; C:membrane fraction; TMS.
 DR GO; GO:0007165; P:signal transduction; TMS.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR010983; EF_Hand_Like.
 DR InterPro; IPR002610; Rhomboid_Like.
 DR Pfam; PF01694; Rhomboid; 1.
 KM Alternative splicing; Hydrolase; Protease; Serine protease;
 KM Transmembrane
 FT TRANSMEM 196 216 Potential.
 FT TRANSMEM 262 282 Potential.
 FT TRANSMEM 284 304 Potential.
 FT TRANSMEM 308 328 Potential.
 FT TRANSMEM 340 359 Potential.
 FT TRANSMEM 372 392 Potential.
 FT TRANSMEM 405 425 Potential.
 FT ACT_SITE 264 264 Charge relay system (By similarity).
 FT ACT_SITE 312 312 Charge relay system (By similarity).
 FT ACT_SITE 377 377 Charge relay system (By similarity).
 FT VARSPLIC 1 77 MGRVEDGTTTELLEDWDPCRSALPARGIKGPREQTGPEL
 FT SCKMRPEPDPSQPGPALMSRGRRARTQALAGSSL -> M
 FT DRSLLQLIOE (in isoform 2).
 FT /FTid=VSP_005372.
 SQ SEQUENCE 438 AA; 48314 MW; A7644AD39644A2F6 CRC64;

Query Match
 Best Local Similarity 96.6%; Score 28; DB 1; Length 438;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPV 6
 DB 304 MRAPV 309

RESULT 15

OBNT69 PRELIMINARY; PRT; 541 AA.
 AC OBNT69; Q6W7S9;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE ResB protein required for cytochrome c biosynthesis (Membrane protein
 required for cytochrome c biosynthesis).
 GN Ordered locus names=Cg10441, cg0523;
 OS Corynebacterium glutamicum (Brevibacterium flavum).
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
 OC NCB1_TaxID=1718;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025 Nakagawa;
 RA Nakagawa S.;
 RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032."
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
 RX PubMed=12948626; DOI=10.1016/S0168-1656(03)00154-8;
 RA Kalinowski J., Bathe B., Bartels D., Bischoff N., Bott M.,
 Burkowski A., Dusch N., Eggeling L., Elkmann B.J., Gaigalat L.,
 Goessmann A., Hartmann M., Huttmacher K., Kraemer R., Linke B.,
 McHardy A.C., Meyer F., Moeckel B., Pfeifferle W., Puhler A.,
 Rey D.A., Rueckert C., Rupp O., Sahn H., Wendisch V.F., Wiegand I.,
 Tauch A.;
 RT "The complete Corynebacterium glutamicum ATCC 13032 genome sequence
 and its impact on the production of L-aspartate-derived amino acids
 and vitamins";
 RL J. Biotechnol. 104:5-25 (2003).
 DR EMBL; AP005275; BAB97834.1; -.
 DR EMBL; BX927149; CAF19157.1; -.
 DR InterPro; IPR007816; ResB.
 DR Pfam; PF05140; ResB; 1.

KM Complete proteome.
 SQ SEQUENCE 541 AA; 61244 MW; 37F42BA0A74F78BB CRC64;
 Query Match
 Best Local Similarity 96.6%; Score 28; DB 2; Length 541;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPV 6
 DB 103 MRAPV 108

Search completed: September 9, 2005, 16:30:38
 Job time: 88.8 secs

DR EMBL: CR543861; CAG68015.1; -
 DR InterPro: IPR007055; TAD.
 DR Pfam: PF04972; BON; 1.
 DR PROSITE: PS50914; BON; 1.
 KW Complete proteome.
 SQ SEQUENCE 231 AA; 24680 MW; 7FCDAFCAD5SL9F CRC64;

Query March 96.6%; Score 28; DB 2; Length 231;
 Best Local Similarity 83.3%; Pred. No. 1.1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPVI 6
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 Db 136 MRAPV 141

RESULT 10
 RHBI_MOUSE STANDARD; PRT; 373 AA.
 AC 08VCG2;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Rhomboid-related protein 1 (EC 3.4.21.-) (RRP) (rhomboid-like protein
 DE 1).
 GN Name=Rhbd1; Synonyms=Rhbd1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Retina;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,
 RA Datchenko L., Matulis K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Pongre C.,
 RA Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Mollary S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whitting M., Madan A., Young A.C., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzyzanski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: May be involved in regulated intramembrane proteolysis
 CC and the subsequent release of functional polypeptides from their
 CC membrane anchors (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -1- SIMILARITY: Belongs to the peptidase S54 family.

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 CC or send an email to license@isb-sib.ch).

DR EMBL: BC021549; AA021549.1; -
 DR MEROPS: S54.005; -
 DR MGD: MGI:2384891; Rhbd1.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR010983; EF_Hand_1like.

DR InterPro: IPR002610; Rhomboid_1like.

DR Pfam: PF01694; Rhomboid; 1.
 KW Hydrolase; Protease; Serine protease; Transmembrane.
 FT TRANSMEM 131 151 Potential.
 FT TRANSMEM 196 216 Potential.
 FT TRANSMEM 219 239 Potential.
 FT TRANSMEM 243 263 Potential.
 FT TRANSMEM 275 294 Potential.
 FT TRANSMEM 307 327 Potential.
 FT TRANSMEM 340 360 Potential.
 FT ACT_SITE 199 199 Charge relay system (By similarity).
 FT ACT_SITE 247 247 Charge relay system (By similarity).
 FT ACT_SITE 312 312 Charge relay system (By similarity).
 SQ SEQUENCE 373 AA; 41786 MW; 1F4E53B83A363DA CRC64;

Query March 96.6%; Score 28; DB 1; Length 373;
 Best Local Similarity 83.3%; Pred. No. 1.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPVI 6
 |||||
 Db 239 MRAPV 244

RESULT 11
 08P9F5 PRELIMINARY; PRT; 376 AA.
 ID 08P9F5;
 AC 08P9F5;
 DT 01-OCT-2002 (TRENBLREL. 22, Created)
 DT 01-OCT-2002 (TRENBLREL. 22, Last sequence update)
 DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
 DE Flagellar protein.
 GN Name=flhB; OrderedLocNames=XCC1910;
 OS Xanthomonas campestris (pv. campestris).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xanthomonas.
 ON NCBI_TaxID=340;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 33913 / NCPPB 528;
 RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
 RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farh C.S., Furlan L.R.,
 RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
 RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
 RA Camarotte G., Camarvan F., Cardoso J., Chambeiro F., Ciapina L.P.,
 RA Ciccarelli R.M.B., Coutinho L.V., Cursino-Santos J.R., El-Dorri H.,
 RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
 RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
 RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
 RA Martins E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Moon D.H.,
 RA Pereira H.A., Rossi A., Senna J.A.D., Silva C., de Souza R.F.,
 RA Spínola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezra R.I.D.,
 RA Trindade dos Santos M., Truffi D., Teal S.M., White F.F.,
 RA Setubal J.C., Kitajima J.P.;
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing
 RT host specificities."

RT host specificities.
 RL Nature 417:459-463(2002).
 CC EMBL: AE012294; AA01199.1; -
 CC DR GO: GO:0016020; C:membrane; IEA.
 CC DR GO: GO:0009306; P:protein secretion; IEA.
 CC DR InterPro: IPR006135; Bac Export_2.
 CC DR InterPro: IPR006136; FlhB.
 CC Pfam: PF01312; Bac_export_2; 1.
 CC DR PRINTS: PR00950; TYPE3JMSPROT.
 CC DR TIGRPFAMs: TIGR00328; flhB; 1.
 KW Complete proteome.
 SQ SEQUENCE 376 AA; 41490 MW; 406778385A158910 CRC64;

Query March 96.6%; Score 28; DB 2; Length 376;
 Best Local Similarity 83.3%; Pred. No. 1.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY      1 MRAPV1 6
      |||||:
Db      285 MRAPV 290

RESULT 12
YTRL_EBV
ID_YTRL_EBV      STANDARD;      PRT;      425 AA.
AC_P30119;
DT      01-APR-1993 (Rel. 25, Created)
DT      01-APR-1993 (Rel. 25, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      Hypothetical BTRF1 protein.
GN      Name=BTRF1;
OS      Epstein-Barr virus (strain B95-8) (HHV-4) (Human herpesvirus 4).
OC      Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC      Gammaherpesvirinae; Lymphocryptovirus.
OX      NCBI_TaxID=10377;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=84270667; PubMed=6087149;
RA      Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
RA      Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,
RA      Tufnell P.S., Barrell B.G.;
RT      "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
RL      Nature 310:207-211(1984).
CC      -1 - SIMILARITY: Belongs to the herpesviruses BTRF1 family.
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CC      -----
CC      EMBL, VO1555; CAA24796.1; -.
DR      PIR; S33045; S33045.
DR      InterPro; IPR006772; Herpes_BTRF1.
DR      Pfam; PF04682; Herpes_BTRF1.
KW      "Hypothetical protein."
SQ      SEQUENCE 425 AA; 46711 MW; 0ECB85FD30495BD CRC64;

Query Match      96.6%; Score 28; DB 1; Length 425;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      1 MRAPV1 6
      |||||:
Db      87 MRAPV1 92

RESULT 13
ID_YTRL_EBV      PRELIMINARY;      PRT;      425 AA.
AC_P30119;
DT      05-JUL-2004 (TrEMBLrel. 27, Created)
DT      05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT      05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE      BTRF1 protein (Fragment).
GN      Name=BTRF1;
OS      Human herpesvirus 4 (Epstein-Barr virus).
OC      Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC      Gammaherpesvirinae; Lymphocryptovirus.
OX      NCBI_TaxID=10376;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=84270667; PubMed=6087149;
RA      Baer R.J., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
RA      Gibson T.J., Hatfull G.F., Hudson G.S., Satchwell S.C., Seguin C.,
RA      Tufnell P.S., Barrell B.G.;

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RT      "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
RL      Nature 310:207-211(1984).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      STRAIN=B95-8;
RX      MEDLINE=88283646; PubMed=2840285;
RA      Laux G., Pericaudet M., Farrell P.J.;
RT      "A spliced Epstein-Barr virus gene expressed in immortalized
RT      lymphocytes is created by circularization of the linear viral
RT      genome.";
RL      EMBO J. 7:769-774(1988).
RN      [3]
RP      SEQUENCE FROM N.A.
RX      STRAIN=B95-8;
RX      MEDLINE=82014887; PubMed=6269068;
RA      Arrand J.R., Rymo L., Walsh J.E., Bjorck E., Lindahl T., Griffin B.E.;
RT      "Molecular cloning of the complete Epstein-Barr virus genome as a set
RT      of overlapping restriction endonuclease fragments.";
RL      Nucleic Acids Res. 9:2999-3014(1981).
RN      [4]
RP      SEQUENCE FROM N.A.
RX      STRAIN=B95-8;
RX      MEDLINE=82059504; PubMed=7301588;
RA      Kozak M.;
RT      "Possible role of flanking nucleotides in recognition of the AUG
RT      initiator codon by eukaryotic ribosomes.";
RL      Nucleic Acids Res. 9:5233-5252(1981).
RN      [5]
RP      SEQUENCE FROM N.A.
RX      STRAIN=B95-8;
RX      MEDLINE=83109311; PubMed=6296170;
RA      Deininger P.L., Bankier A., Farrell P., Baer R., Barrell B.;
RT      "Sequence analysis and in vitro transcription of portions of the
RT      Epstein-Barr virus genome.";
RL      J. Cell. Biochem. 19:267-274(1982).
RN      [6]
RP      SEQUENCE FROM N.A.
RX      STRAIN=B95-8;
RX      MEDLINE=83169725; PubMed=6300857;
RA      Farrell P.J., Deininger P.L., Bankier A., Barrell B.;
RT      "Homologous upstream sequences near Epstein-Barr virus promoters.";
RL      Proc. Natl. Acad. Sci. U.S.A. 80:1565-1569(1983).
RN      [7]
RP      SEQUENCE FROM N.A.
RX      STRAIN=B95-8;
RX      MEDLINE=85035713; PubMed=6092825;
RA      Bankier A.T., Deininger P.L., Farrell P.J., Barrell B.G.;
RT      "Sequence analysis of the 17,166 base-pair EcoRI fragment C of B95-8
RT      Epstein-Barr virus.";
RL      Mol. Biol. Med. 1:21-45(1983).
RN      [8]
RP      SEQUENCE FROM N.A.
RX      STRAIN=B95-8;
RX      MEDLINE=85060424;
RA      Seguin C., Farrell P.J., Barrell B.G.;
RT      "DNA sequence and transcription of the BamHI fragment B region of B95-
RT      8 Epstein-Barr virus.";
RL      Mol. Biol. Med. 1:369-392(1983).
RN      [9]
RP      SEQUENCE FROM N.A.
RX      STRAIN=B95-8;
RX      MEDLINE=83294686; PubMed=6310141;
RA      Jeang K.T., Hayward S.D.;
RT      "Organization of the Epstein-Barr virus DNA molecule. III. Location of
RT      the P3HR-1 deletion junction and characterization of the NotI repeat
RT      units that form part of the template for an abundant 12-O-
RT      tetradecanoylphorbol-13-acetate-induced mRNA transcript.";
RL      J. Virol. 48:135-148(1983).
RN      [10]
RP      SEQUENCE FROM N.A.
RX      STRAIN=B95-8;
RX      MEDLINE=85060428; PubMed=6094955;
RA      Bankier A.T., Deininger P.L., Satchwell S.C., Baer R., Farrell P.J.,

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DR InterPro: IPR004100; ATPase a/b_N.
 DR InterPro: IPR005714; Pili_yescN.
 DR Pfam: PF00006; ATP-8ynt_ab; 1.
 DR SMART: SM00382; AAA; 1.
 DR TIGRFAMs: TIGR01026; fliI_yescN; 1.
 DR PROSITE: PS00152; ATPase ALPHA BETA; UNKNOWN 1.
 DR ATP synthetase; ATP-binding; Hydrolase; Ion transport; Transport.
 SO SEQUENCE 442 AA; 46813 MW; AD070DD4E17FD3CC3 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 442;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPV1 6
 DB 77 MRAPV1 82

RESULT 5
 ID 061371 PRELIMINARY; PRT; 629 AA.
 AC 061371; Q9TXV7;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Fecylcholinesesterase (EC 3.1.1.7) (Abnormal acetylcholinesesterase
 DE protein 2).
 GN Nameace-2; ORFNames=Y44E3A.2;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Paloderinae; Caenorhabditis.
 OX NCBI_Taxid=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=N2;
 RX MEDLINE=98198570; PubMed=9539167; DOI=10.1016/S0014-5793(98)00191-4;
 RA Grauso M., Culetto E., Combes D., Fedon Y., Tountant J.P., Arpagaus M.;
 RT "Existence of four acetylcholinesesterase genes in the nematodes
 RT Caenorhabditis elegans and Caenorhabditis briggsae.";
 RL FEBS Lett. 424:279-284(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=N2;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RG WormBase Consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Woessner J., Graves T., Keppeler D.;
 RT "The sequence of C. elegans coemid Y44E3A.";
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Wilson R.;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RG WormBase Consortium;

RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 DR EMBL: AF025378; AAC14016.2; -.
 DR EMBL: AF106589; AAC78228.2; -.
 DR PIR: T33842; T33842.
 DR PIR: T37255; T37255.
 DR HSSP: P06276; 1P0P.
 DR WormBase; WBGene00000036; ace-2.
 DR WormPep; Y44E3A.2; CE28363.
 DR GO; GO:0003990; F:acetylcholinesesterase activity; IEA.
 DR GO; GO:0004104; F:cholinesesterase activity; IEA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR InterPro: IPR002018; CarpesteraseB.
 DR InterPro: IPR000997; Cholinesterase.
 DR InterPro: IPR000379; Ser esters.
 DR Pfam: PF00135; Coesterase; 1.
 DR PRINTS: PR00878; CHOLINESTRASE.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
 KW Hydrolase.
 SO SEQUENCE 629 AA; 70863 MW; 74940F512FEDF869 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 629;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPV1 6
 DB 1 MRAPV1 6

RESULT 6
 ID 06PD31 PRELIMINARY; PRT; 939 AA.
 AC 06PD31;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalski U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC058971; AAH58971.1; -.
 DR InterPro: IPR006933; HAP1_N.

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DR InterPro; IPR000585; Hemopexin.
DR Pfam; PF04849; HAP1_N; 1.
DR PROSITE; PS00024; HEMOPEXIN; UNKNOWN_1.
DR Hypothetical protein.
SQ SEQUENCE 939 AA; 104466 MW; 64B1D5D34DF36FCB CRC64;

Query Match
Best Local Similarity 100.0%; Score 29; DB 2; Length 939;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRAPV 6
Db 924 MRAPV 921

RESULT 7
O80TL6 PRELIMINARY; PRT; 947 AA.
AC O80TL6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MKIA1042 protein (Fragment).
GN Name=mkIA1042;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=22579291; PubMed=12693553;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S.,
RA Nakajima D., Nagase T., Ohara O., Koga H.;
RT Prediction of the coding sequences of mouse homologues of KIAA gene:
RT I. The complete nucleotide sequences of 400 mouse KIAA-homologous
RT cDNAs identified by screening of terminal sequences of cDNA clones
RT randomly sampled from size-fractionated libraries."
RL DNA Ref. 10:35-48(2003).
DR EMBL; AK122426; BAC65708.1; -.
DR GO; GO:0005634; Cytoplasm; ISS.
DR GO; GO:0005886; Cytoplasmic membrane; ISS.
DR GO; GO:0005515; Protein binding; ISS.
DR GO; GO:0005102; Receptor binding; ISS.
DR GO; GO:0006493; P-O-linked glycosylation; ISS.
DR GO; GO:0006605; Protein targeting; ISS.
DR GO; GO:0006357; Regulation of transcription from Pol II pro. .; ISS.
DR InterPro; IPR006933; HAP1_N.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR010978; cRNA_binding_arm.
DR Pfam; PF04849; HAP1_N; 1.
DR PROSITE; PS00024; HEMOPEXIN; UNKNOWN_1.
FT NON TER
SQ SEQUENCE 947 AA; 105486 MW; 0987284C6ACF23A5 CRC64;

Query Match
Best Local Similarity 100.0%; Score 29; DB 2; Length 947;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRAPV 6
Db 924 MRAPV 929

RESULT 8
RHBI_RAT
ID RHBI_RAT STANDARD; PRT; 164 AA.
AC O88779;
DT 28-FEB-2003 (rel. 41, Created)
DT 28-FEB-2003 (rel. 41, Last sequence update)
DT 25-OCT-2004 (rel. 45, Last annotation update)
DE Rhomboid-related protein 1 (EC 3.4.21.-) (RR) (Rhomboid-like protein

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DE 1) (Fragment).
GN Name=Rbdl1; Synonym=Rhbd1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Intestinal epithelium;
RC MEDLINE=96324821; PubMed=9662444; DOI=10.1016/S0014-5793(98)00622-X;
RA Pascual J.C., Brown K.D.;
RT "Characterization of a mammalian cDNA encoding a protein with high
RT sequence similarity to the Drosophila regulatory protein Rhomboid."
RT FEBS Lett. 429:337-340(1998).
CC -1- FUNCTION: May be involved in regulated intramembrane proteolysis
CC and the subsequent release of functional polypeptides from their
CC membrane anchors (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the peptidase S54 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (see http://www.isb-sdb.ch/announce/
CC or send an email to license@isb-sdb.ch).
CC -----
DR EMBL; Y17258; CAA76716.1; -.
DR MEROPS; S54.005; -.
DR InterPro; IPR002610; Rhomboid_like.
DR Pfam; PF01694; Rhomboid; 1.
KM Hydrolyase; Protease; Serine protease; Transmembrane.
FT NON TER
FT TRANSMEM 1 30 Potential.
FT TRANSMEM 32 52 Potential.
FT TRANSMEM 56 76 Potential.
FT TRANSMEM 120 140 Potential.
FT ACT SITE 60 60 Charge relay system (By similarity).
FT ACT SITE 125 125 Charge relay system (By similarity).
FT NON TER 164 164
SQ SEQUENCE 164 AA; 17662 MW; CF62ACE3B6C99210 CRC64;

Query Match
Best Local Similarity 96.6%; Score 28; DB 1; Length 164;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRAPV 6
Db 52 MRAPV 57

RESULT 9
O6FD44 PRELIMINARY; PRT; 231 AA.
AC O6FD44;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=ACIAD1133;
OS Acinetobacter sp. (strain ADP1).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxId=62977;
RN [1]
RP SEQUENCE FROM N.A.
RA Barbe V., Vallenc D., Fonknechten N., Kreilmeyer A., Oztas S.,
RA Labarre L., Crussatier S., Robert C., Duprat S., Wincker P.,
RA Orsillon L.N., Weissenbach J., Marliere P., Cohen G.N., Medigue C.;
RT "Unique features revealed by the genome sequence of Acinetobacter sp.
RT ADP1, a versatile and naturally transformation competent bacterium."
RT Nucleic Acids Res. 0:0-0(2004).

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OM protein - protein search, using sw model

Run on: September 9, 2005, 15:47:04 ; Search time 24 Seconds
(without alignments)
18.662 Million cell updates/sec

Title: US-10-032-037C-8

Perfect score: 29

Sequence: 1 MRAPV1 6

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 7464964 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

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- 2: /cgn2_6/prodata/1/aa/5B COMB pep:*
- 3: /cgn2_6/prodata/1/aa/5A COMB pep:*
- 4: /cgn2_6/prodata/1/aa/5B COMB pep:*
- 5: /cgn2_6/prodata/1/aa/5A COMB pep:*
- 6: /cgn2_6/prodata/1/aa/5B COMB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	96.6	973	4 US-09-252-991A-23944	Sequence 23944, A
2	26	89.7	229	4 US-09-248-796A-16460	Sequence 16460, A
3	26	89.7	286	4 US-09-711-164-385	Sequence 185, App
4	26	89.7	350	4 US-09-198-452A-643	Sequence 643, App
5	26	89.7	350	4 US-09-438-185A-605	Sequence 605, App
6	26	89.7	477	4 US-09-489-039A-8906	Sequence 8906, App
7	25	86.2	119	4 US-09-252-991A-28425	Sequence 28425, A
8	25	86.2	120	4 US-09-107-532A-6688	Sequence 6688, App
9	25	86.2	197	4 US-09-902-540-13013	Sequence 13013, A
10	25	86.2	222	4 US-09-489-039A-8244	Sequence 8244, App
11	25	86.2	222	4 US-09-538-092-272	Sequence 272, App
12	25	86.2	223	4 US-09-134-000C-6010	Sequence 6010, App
13	25	86.2	224	4 US-09-538-092-617	Sequence 617, App
14	25	86.2	233	4 US-09-489-039A-7366	Sequence 7366, App
15	25	86.2	239	4 US-09-328-352-5866	Sequence 5866, App
16	25	86.2	231	4 US-09-602-777A-36	Sequence 36, App
17	25	86.2	319	4 US-09-252-991A-19964	Sequence 19964, A
18	25	86.2	437	4 US-09-270-767-44567	Sequence 44567, A
19	25	86.2	451	4 US-09-252-991A-26783	Sequence 26783, A
20	25	86.2	489	4 US-09-489-039A-10515	Sequence 10515, A
21	25	86.2	487	4 US-09-583-110-3569	Sequence 3569, App
22	25	86.2	488	4 US-09-107-433-3552	Sequence 3552, App
23	25	86.2	657	4 US-09-252-991A-27682	Sequence 27682, A
24	25	86.2	885	4 US-09-902-540-13431	Sequence 13431, A
25	25	86.2	962	4 US-09-328-352-7942	Sequence 7942, App
26	24	82.8	73	4 US-09-621-976-6392	Sequence 6392, App
27	24	82.8	76	4 US-09-636-215-575	Sequence 575, App

28	24	82.8	76	4 US-09-685-166A-575	Sequence 575, App
29	24	82.8	76	4 US-09-685-166A-888	Sequence 888, App
30	24	82.8	76	4 US-09-679-426-575	Sequence 575, App
31	24	82.8	76	4 US-09-679-426-888	Sequence 888, App
32	24	82.8	76	4 US-09-759-143-575	Sequence 575, App
33	24	82.8	76	4 US-09-759-143-888	Sequence 888, App
34	24	82.8	76	4 US-09-651-236-575	Sequence 575, App
35	24	82.8	82	3 US-09-134-001C-4676	Sequence 4676, App
36	24	82.8	89	3 US-09-134-001C-4563	Sequence 4563, App
37	24	82.8	93	4 US-09-938-806A-8	Sequence 8, App
38	24	82.8	102	4 US-09-248-796A-14433	Sequence 14433, A
39	24	82.8	108	4 US-09-513-999C-5944	Sequence 5944, App
40	24	82.8	125	3 US-09-199-637A-403	Sequence 403, App
41	24	82.8	125	4 US-09-269-410-11	Sequence 11, App
42	24	82.8	125	4 US-09-513-999C-5838	Sequence 5838, App
43	24	82.8	143	4 US-09-270-767-42631	Sequence 42631, A
44	24	82.8	162	3 US-08-801-742-3	Sequence 3, App
45	24	82.8	192	1 US-08-208-008C-9	Sequence 9, App

ALIGNMENTS

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RESULT 1
US-09-252-991A-23944
Sequence 23944, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfeld et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23944
LENGTH: 973
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23944

Query Match          96.6%; Score 28; DB 4; Length 973;
Best Local Similarity 83.3%; Pred. 46+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRAPV1 6
Db      387 MRAPV1 392

RESULT 2
US-09-248-796A-16460
Sequence 16460, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
PRIOR FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 16460
LENGTH: 229
TYPE: PRT
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; ORGANISM: Candida albicans
; US-09-248-796a-16460

Query Match 89.7%; Score 26; DB 4; Length 229;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPVI 6
|:||||
Db 182 MKAPVI 187

RESULT 3
US-09-711-164-385

; Sequence 385, Application US/09711164
; Patent No. 6589738
; GENERAL INFORMATION:
; APPLICANT: Forsyth, R. Allyn
; APPLICANT: Olsen, Karl
; APPLICANT: Zyskind, Judith
; TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERET
; FILE REFERENCE: ELITRA.008A
; CURRENT APPLICATION NUMBER: US/09/711,164
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/164415
; PRIOR FILING DATE: 1999-11-9
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 385
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Escherichia coli
; US-09-711-164-385

Query Match 89.7%; Score 26; DB 4; Length 286;
Best Local Similarity 83.3%; Pred. No. 3.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPVI 6
|:||||
Db 41 MRSPVI 46

RESULT 4
US-09-198-452a-643

; Sequence 643, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 643
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; US-09-198-452a-643

Query Match 89.7%; Score 26; DB 4; Length 350;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPVI 6
|:||||
Db 109 LRAPVI 114

RESULT 5
US-09-438-185a-605

; Sequence 605, Application US/09438185A
; Patent No. 6822071

; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kalman, Sue
; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 605
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CPN0603
; US-09-438-185a-605

Query Match 89.7%; Score 26; DB 4; Length 350;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPVI 6
|:||||
Db 109 LRAPVI 114

RESULT 6
US-09-489-039a-8906

; Sequence 8906, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8906
; LENGTH: 477
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039a-8906

Query Match 89.7%; Score 26; DB 4; Length 477;
Best Local Similarity 83.3%; Pred. No. 5.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPVI 6
|:||||
Db 269 MKAPVI 274

RESULT 7
US-09-252-991a-28425

; Sequence 28425, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUDINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136

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; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28425
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-28425

Query Match
Best Local Similarity 86.2%; Score 25; DB 4; Length 119;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRAPI 6
Db 63 MRAPI 68

RESULT 8
US-09-107-532A-6688
; Sequence 6688, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS: GENOME THERAPEUTICS CORPORATION
; ADDRESSER: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Arinello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 893-5007
; TELEFAX: (781) 893-8277
; INFORMATION FOR SEQ ID NO: 6688:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULAR TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...120
; SEQUENCE DESCRIPTION: SEQ ID NO: 6688:
US-09-107-532A-6688

Query Match
Best Local Similarity 86.2%; Score 25; DB 4; Length 120;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 6
Db 17 MRAPI 22

RESULT 9
US-09-902-540-13013
; Sequence 13013, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: MYXOCOCCUS XANTHUS Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 13013
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
; US-09-902-540-13013

Query Match
Best Local Similarity 86.2%; Score 25; DB 4; Length 197;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 5
Db 1 MRAPI 5

RESULT 10
US-09-489-039A-8244
; Sequence 8244, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8244
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039A-8244

Query Match
Best Local Similarity 86.2%; Score 25; DB 4; Length 222;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 5
Db 24 MRAPI 28

RESULT 11
US-09-538-092-272
; Sequence 272, Application US/09538092
; Patent No. 6753314
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; GENERAL INFORMATION:
; APPLICANT: Glot, Loic
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 272
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number YFL060C
US-09-538-092-272
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Query Match      86.2%; Score 25; DB 4; Length 222;
Best Local Similarity 83.3%; Pred. No. 3.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1  MRAPV 6
        :|||||
Db      151  IRAPV 156
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RESULT 12
US-09-134-000C-6010
; Sequence 6010, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6010
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6010
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Query Match      86.2%; Score 25; DB 4; Length 223;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1  MRAPV 5
        :|||||
Db      127  MRAPV 131
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RESULT 13
US-09-538-092-617
; Sequence 617, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Loic
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
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; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 617
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number YMR095C
US-09-538-092-617
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Query Match      86.2%; Score 25; DB 4; Length 224;
Best Local Similarity 83.3%; Pred. No. 4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1  MRAPV 6
        :|||||
Db      160  IRAPV 165
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RESULT 14
US-09-489-039A-7366
; Sequence 7366, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709,2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7366
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7366
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Query Match      86.2%; Score 25; DB 4; Length 233;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1  MRAPV 5
        :|||||
Db      173  MRAPV 177
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RESULT 15
US-09-328-352-5866
; Sequence 5866, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5866
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5866
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Query Match      86.2%; Score 25; DB 4; Length 239;
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Best Local Similarity 66.7%; Pred. No. 4.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 6
|:|:|:
Db 140 MKAPV 145

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Job time : 26 secs

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OM protein - protein search, using sw model

Run on: September 9, 2005, 15:52:48 ; Search time 91.5 Seconds

(without alignments)
25.864 Million cell updates/sec

Title: US-10-032-037C-8

Perfect score: 29

Sequence: 1 MRAPV1 6

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	6	US-10-032-037B-8	Sequence 8, Appli
2	29	100.0	6	US-10-029-988B-8	Sequence 8, Appli
3	29	100.0	6	US-10-032-423A-8	Sequence 8, Appli
4	29	100.0	6	US-10-029-926B-8	Sequence 8, Appli
5	29	100.0	6	US-10-610-843B-4	Sequence 2, Appli
6	29	100.0	6	US-10-611-588C-2	Sequence 4, Appli
7	29	100.0	6	US-10-880-922-4	Sequence 4, Appli
8	29	100.0	6	US-10-032-037B-204	Sequence 204, App
9	29	100.0	266	US-10-029-988B-204	Sequence 204, App
10	29	100.0	266	US-10-032-423A-204	Sequence 204, App
11	29	100.0	277	US-10-032-037B-25	Sequence 25, Appli

12	29	100.0	277	US-10-029-988B-25	Sequence 25, Appli
13	29	100.0	277	US-10-032-423A-25	Sequence 25, Appli
14	29	100.0	277	US-10-029-926B-25	Sequence 25, Appli
15	29	100.0	277	US-10-610-843B-1	Sequence 1, Appli
16	29	100.0	277	US-10-610-843B-2	Sequence 2, Appli
17	29	100.0	280	US-10-610-843B-3	Sequence 3, Appli
18	29	100.0	280	US-10-611-588C-1	Sequence 1, Appli
19	29	100.0	442	US-10-369-493-7871	Sequence 7871, Ap
20	29	100.0	464	US-10-032-037B-26	Sequence 26, Appli
21	29	100.0	464	US-10-029-988B-26	Sequence 26, Appli
22	29	100.0	464	US-10-032-423A-26	Sequence 26, Appli
23	29	100.0	464	US-10-029-926B-26	Sequence 26, Appli
24	29	100.0	86	US-10-424-599-253048	Sequence 253048,
25	28	96.6	123	US-10-424-599-150638	Sequence 150638,
26	28	96.6	343	US-10-263-367-12	Sequence 12, Appli
27	28	96.6	438	US-09-908-419-2	Sequence 2, Appli
28	28	96.6	438	US-10-056-790-2	Sequence 36, Appli
29	28	96.6	438	US-10-056-790-36	Sequence 11, Appli
30	28	96.6	438	US-10-477-505A-11	Sequence 46, Appli
31	28	96.6	470	US-10-056-790-46	Sequence 3996, Ap
32	28	96.6	541	US-09-738-626-3996	Sequence 273558,
33	27	93.1	99	US-10-424-599-272558	Sequence 294304,
34	26	89.7	74	US-10-425-115-294304	Sequence 42410, A
35	26	89.7	112	US-10-767-701-42410	Sequence 7418, Ap
36	26	89.7	126	US-10-032-585-7418	Sequence 335198,
37	26	89.7	258	US-10-425-115-335198	Sequence 385, App
38	26	89.7	286	US-10-287-274-385	Sequence 43216, A
39	26	89.7	286	US-10-369-493-23563	Sequence 335200,
40	26	89.7	288	US-10-282-122A-43216	Sequence 69148, A
41	26	89.7	288	US-10-425-115-335200	Sequence 55193, A
42	26	89.7	290	US-10-282-122A-61193	Sequence 55531, A
43	26	89.7	319	US-10-425-114-55531	Sequence 45307, A
44	26	89.7	319	US-10-425-114-55531	
45	26	89.7	345	US-10-767-701-45307	

ALIGNMENTS

RESULT 1
US-10-032-037B-8
; Sequence 8, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y11-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032, 037B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258, 948
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-8

Query Match
Best Local Similarity 100.0%; Score 29; DB 15; Length 6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPV1 6
|||||
Db 1 MRAPV1 6

RESULT 2
US-10-029-988B-8
; Sequence 8, Application US/10029988B
; Publication No. US20040001839A1

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/ GENERAL INFORMATION:
/ APPLICANT: Bio-Technology General Corp.
/ TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
/ MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
/ FILE REFERENCE: 10793/46
/ CURRENT APPLICATION NUMBER: US/10/029,988B
/ PRIOR FILING DATE: 2001-12-31
/ PRIOR APPLICATION NUMBER: 60/258,948
/ PRIOR FILING DATE: 2000-12-29
/ NUMBER OF SEQ ID NOS: 204
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 8
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-029-988B-8

Query Match      100.0%; Score 29; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRAPVI 6
        |||||
        1 MRAPVI 6

Db

RESULT 3
US-10-032-423A-8
/ Sequence 8, Application US/10032423A
/ Publication No. US20040002450A1
/ GENERAL INFORMATION:
/ APPLICANT: Bio-Technology General Corp.
/ TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
/ MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
/ FILE REFERENCE: 10793/45
/ CURRENT APPLICATION NUMBER: US/10/032,423A
/ PRIOR FILING DATE: 2001-12-31
/ PRIOR APPLICATION NUMBER: 60/258,948
/ PRIOR FILING DATE: 12/29/2000
/ NUMBER OF SEQ ID NOS: 204
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 8
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-032-423A-8

Query Match      100.0%; Score 29; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRAPVI 6
        |||||
        1 MRAPVI 6

Db

RESULT 4
US-10-029-926B-8
/ Sequence 8, Application US/10029926B
/ Publication No. US20040073011A1
/ GENERAL INFORMATION:
/ APPLICANT: Hgavy, et al.
/ TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
/ FILE REFERENCE: 10793/50
/ CURRENT APPLICATION NUMBER: US/10/029,926B
/ PRIOR FILING DATE: 2001-12-31
/ PRIOR APPLICATION NUMBER: 60/258,948
/ PRIOR FILING DATE: 12/29/2000
/ NUMBER OF SEQ ID NOS: 203
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 8
/ LENGTH: 6
/ TYPE: PRT
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/ ORGANISM: Homo sapiens
US-10-029-926B-8

Query Match      100.0%; Score 29; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRAPVI 6
        |||||
        1 MRAPVI 6

Db

RESULT 5
US-10-610-843B-4
/ Sequence 4, Application US/10610843B
/ Publication No. US2004020265A1
/ GENERAL INFORMATION:
/ APPLICANT: Lazarovits, et al.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPEUTIC TREATMENT
/ FILE REFERENCE: 10793/72
/ CURRENT APPLICATION NUMBER: US/10/610,843B
/ PRIOR FILING DATE: 2003-06-30
/ PRIOR APPLICATION NUMBER: 60/393,453
/ PRIOR FILING DATE: 2002-07-01
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 4
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-610-843B-4

Query Match      100.0%; Score 29; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRAPVI 6
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        1 MRAPVI 6

Db

RESULT 6
US-10-611-588C-2
/ Sequence 2, Application US/10611588C
/ Publication No. US2004020887A1
/ GENERAL INFORMATION:
/ APPLICANT: Levanon, et al.
/ TITLE OF INVENTION: ANTIBODIES AND USES THEREOF
/ FILE REFERENCE: 10793/70
/ CURRENT APPLICATION NUMBER: US/10/611,588C
/ CURRENT FILING DATE: 2003-06-30
/ PRIOR APPLICATION NUMBER: 60/393,491
/ PRIOR FILING DATE: 2002-07-01
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 2
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-611-588C-2

Query Match      100.0%; Score 29; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRAPVI 6
        |||||
        1 MRAPVI 6

Db

RESULT 7
US-10-880-922-4
/ Sequence 4, Application US/10880922
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; Publication No. US20050069955A1
; GENERAL INFORMATION:
; APPLICANT: PIAKSIN, DANIEL
; APPLICANT: LEVANO, AVIGDOR
; APPLICANT: SZANTON, ESTHER
; APPLICANT: HAGAY, YOCHVED
; APPLICANT: BEN-LEVY, RACHEL
; APPLICANT: NISGAV, YAEI
; APPLICANT: KANFI, YARIV
; TITLE OF INVENTION: ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 10793-143
; CURRENT APPLICATION NUMBER: US/10/880,922
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/484,061
; PRIOR FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Patent In Ver. 3.2
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-880-922-4

Query Match      100.0%; Score 29; DB 17; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MRAPI 6
Db      1 MRAPI 6

RESULT 8
US-10-032-037B-204
; Sequence 204, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 204
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-204

Query Match      100.0%; Score 29; DB 15; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MRAPI 6
Db      121 MRAPI 126

RESULT 9
US-10-029-988B-204
; Sequence 204, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
```

```

; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 204
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-204

Query Match      100.0%; Score 29; DB 15; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MRAPI 6
Db      121 MRAPI 126

RESULT 10
US-10-032-423A-204
; Sequence 204, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 204
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-204

Query Match      100.0%; Score 29; DB 15; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MRAPI 6
Db      121 MRAPI 126

RESULT 11
US-10-032-037B-25
; Sequence 25, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-25
```

Query Match 100.0%; Score 29; DB 15; Length 277;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
|||||
Db 121 MRAPVI 126

RESULT 12

US-10-029-988B-25
; Sequence 25, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 277
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-029-988B-25

Query Match 100.0%; Score 29; DB 15; Length 277;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
|||||
Db 121 MRAPVI 126

RESULT 13

US-10-032-423A-25
; Sequence 25, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 277
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-032-423A-25

Query Match 100.0%; Score 29; DB 15; Length 277;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
|||||
Db 121 MRAPVI 126

RESULT 14

US-10-029-926B-25
; Sequence 25, Application US/10029926B
; Publication No. US20040073011A1

; GENERAL INFORMATION:
; APPLICANT: HEGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 277
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-029-926B-25

Query Match 100.0%; Score 29; DB 15; Length 277;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
|||||
Db 121 MRAPVI 126

RESULT 15

US-10-610-843B-1
; Sequence 1, Application US/10610843B
; Publication No. US20040202665A1
; GENERAL INFORMATION:
; APPLICANT: Lazarovits, et al.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPEUTIC TREATMENT
; FILE REFERENCE: 10793/72
; CURRENT APPLICATION NUMBER: US/10/610,843B
; PRIOR FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: 60/393,453
; PRIOR FILING DATE: 2002-07-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 277
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-610-843B-1

Query Match 100.0%; Score 29; DB 16; Length 277;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
|||||
Db 121 MRAPVI 126

Search completed: September 9, 2005, 16:18:17
Job time : 92.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 9, 2005, 15:56:35 ; Search time 107.45 Seconds
(without alignments)
25.196 Million cell updates/sec

Title: US-10-032-037C-266

Perfect score: 44

Sequence: 1 YDYPERE 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	7	5	ABG92031
2	44	100.0	13	2	AAW14607
3	44	100.0	13	5	ABG92050
4	44	100.0	13	5	ABG92029
5	44	100.0	13	8	ADJ57380
6	44	100.0	14	2	AAW14607
7	44	100.0	15	2	AAW14607
8	44	100.0	15	2	AAW14607
9	44	100.0	16	2	AAW14607
10	44	100.0	18	5	ABG92048
11	44	100.0	18	5	ABG92048
12	44	100.0	18	5	ABG92057
13	44	100.0	18	8	ADJ57379
14	44	100.0	19	5	ABG92028
15	44	100.0	19	5	ABG92052
16	44	100.0	21	2	AAW14607
17	44	100.0	21	2	AAW14607
18	44	100.0	24	2	AAW14607
19	44	100.0	60	2	AAW14607
20	44	100.0	61	2	AAW14607
21	44	100.0	63	2	AAW14607
22	44	100.0	66	4	AAW14607
23	44	100.0	66	4	AAW14607
24	44	100.0	67	2	AAW14607
25	44	100.0	290	5	ABW78244

26	44	100.0	290	5	ABW78243	AbW78243 Amino aci
27	44	100.0	290	5	ABW78245	AbW78245 Amino aci
28	44	100.0	293	1	AAW14607	AAW14607 45 Kda am
29	44	100.0	300	5	ABW78240	AbW78240 Amino aci
30	44	100.0	301	5	ABW78241	AbW78241 Amino aci
31	44	100.0	302	5	ABW78242	AbW78242 Amino aci
32	44	100.0	531	5	ABW78238	AbW78238 Amino aci
33	44	100.0	531	5	ABW78239	AbW78239 Amino aci
34	44	100.0	531	5	ABW78237	AbW78237 Amino aci
35	44	100.0	544	5	ABW78236	AbW78236 Amino aci
36	44	100.0	544	5	ABW78235	AbW78235 Amino aci
37	44	100.0	544	5	ABW78234	AbW78234 Amino aci
38	44	100.0	562	3	AAW14607	AAW14607 Human gly
39	44	100.0	568	3	AAW14607	AAW14607 Human gly
40	44	100.0	610	2	AAW14607	AAW14607 Mutant pl
41	44	100.0	610	2	AAW14607	AAW14607 Platelet
42	44	100.0	610	2	AAW14607	AAW14607 Mutated p
43	44	100.0	626	4	AAW14607	AAW14607 Platelet
44	44	100.0	626	4	AAW14607	AAW14607 Human gly
45	44	100.0	626	7	ADW69094	ADW69094 Human MPS

ALIGNMENTS

RESULT 1	ABG92031	standard; peptide; 7 AA.
ID	ABG92031	
AC	ABG92031	
XX		
DT	04-DEC-2002	(first entry)
XX		
DE	Human epitope sequence #5.	
XX		
KM	Human; epitope; cancer; tumour; cell rolling; inflammation; metastasis;	
KW	hypervariable region; autoimmune disease; thrombosis; restenosis;	
KM	leukemia; inflammatory disease; cardiovascular disease;	
KW	myocardial infarction; retinopathic disease; abnormal platelet function;	
KM	sulphated tyrosine-dependent protein-protein interaction.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200253700-A2.	
XX		
PD	11-JUL-2002.	
XX		
PF	31-DEC-2001; 2001WO-US049442.	
XX		
PR	29-DEC-2000; 2000US-00751181.	
XX		
PR	29-DEC-2000; 2000US-0258948P.	
XX		
PA	(BIOT-) BIO-TECHNOLOGY GEN CORP.	
XX		
PI	Lazarovits J, Hagai Y, Plakshin D, Vogel T, Nimrod A, Mar-Haim H;	
PI	Szantonon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;	
XX		
DR	WPI; 2002-674776/72.	
XX		
PT	Novel isolated epitope present on cancer cells and important in	
PT	physiological phenomena such as cell rolling, metastasis and	
PT	inflammation, for treating autoimmune, inflammatory or cardiovascular	
PT	diseases, and cancer.	
XX		
PS	Claim 43; Page 132; OP; English.	
XX		
CC	The invention relates to an isolated epitope present on cancer cells and	
CC	important in physiological phenomena such as cell rolling, metastasis and	
CC	inflammation, where the epitope is capable of being bound by an antibody,	
CC	its antigen-binding fragment or its complex comprising at least one	
CC	antibody or its binding fragment having a first hypervariable region. The	
CC	epitopes are useful for inhibiting cell rolling, inflammation, autoimmune	
CC	disease, thrombosis, restenosis, metastasis, growth and/or replication of	

CC tumour or leukaemia cells, increase in number of tumour or leukaemia
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing
 CC mortality of tumour or leukaemia cells, for increasing the susceptibility
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-
 CC leukaemia agents, or for decreasing the number of tumour or leukaemia
 CC cells in a patient, or in the manufacture of a medicament for the above
 CC mentioned purposes. The epitopes are useful for diagnosing and treating
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
 CC diseases, cardiovascular diseases such as myocardial infarction,
 CC retinopathic diseases and other diseases mediated by abnormal platelet
 CC function and diseases caused by sulphated tyrosine-dependent protein-
 CC protein interactions. This sequence represents a human epitope sequence
 CC of the invention
 CC
 CC

SQ Sequence 7 AA;

Query Match 100.0%; Score 44; DB 5; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YDYYPEE 7
 DB 1 YDYYPEE 7

RESULT 2
 AA014607

ID AA014607 standard; peptide; 13 AA.

AC AA014607;

DT 09-DEC-1997 (first entry)

XX Human antithrombin III carboxy-terminal extension.

XX Human; antithrombin III; mutant; carboxy-terminal; extension;

XX sulphated tyrosine; prevention; treatment; thrombosis; disease.

XX Synthetic.

OS Key Location/Qualifiers

FT Region 1..3
 FT /note="carboxy-terminus of wild type human antithrombin
 FT III"

PN JP09071600-A.

PD 18-MAR-1997.

XX 06-SEP-1995; 95JP-00228694.

PR 06-SEP-1995; 95JP-00228694.

PA (EISA) EISAI CO LTD.

DR WPI; 1997-231188/21.

PT Human antithrombin III mutant with C-terminal peptide containing a
 PT sulphated tyrosine - useful for treatment and prevention of thrombotic
 PT disease.

XX Disclosure; Page 6; 11pp; Japanese.

CC A human antithrombin III (AT III) mutant, comprising a carboxy-terminal
 CC sulphated tyrosine peptide extension, i.e. the present peptide, can be
 CC used to prevent and/or treat thrombotic diseases
 CC
 CC

SQ Sequence 13 AA;

Query Match 100.0%; Score 44; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.74;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YDYYPEE 7
 DB 4 YDYYPEE 10

RESULT 3
 ABG92050

ID ABG92050 standard; peptide; 13 AA.

AC ABG92050;

DT 04-DEC-2002 (first entry)

XX Human epitope sequence #23.

XX Human; epitope; cancer; tumour; cell rolling; inflammation; metastasis;
 KW hypervariable region; autoimmune disease; thrombosis; restenosis;
 KW leukaemia; inflammatory disease; cardiovascular disease;
 KW myocardial infarction; retinopathic disease; abnormal platelet function;
 KW sulphated tyrosine-dependent protein-protein interaction.

OS Homo sapiens.

PN WO200253700-A2.

PD 11-JUL-2002.

PF 31-DEC-2001; 2001WO-US049442.

PR 29-DEC-2000; 2000US-00751181.

PR 29-DEC-2000; 2000US-0258948P.

PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
 PI Szanton J, Richter T, Amlt B, Kooperman L, Peretz T, Levanon A;

DR WPI; 2002-674776/72.

PT Novel isolated epitope present on cancer cells and important in
 PT physiological phenomena such as cell rolling, metastasis and
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular
 PT diseases, and cancer.

PS Disclosure; Page 60; 0pp; English.

XX The invention relates to an isolated epitope present on cancer cells and
 CC important in physiological phenomena such as cell rolling, metastasis and
 CC inflammation, where the epitope is capable of being bound by an antibody,
 CC its antigen-binding fragment or its complex comprising at least one
 CC antibody or its binding fragment having a first hypervariable region. The
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing
 CC mortality of tumour or leukaemia cells, for increasing the susceptibility
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-
 CC leukaemia agents, or for decreasing the number of tumour or leukaemia
 CC cells in a patient, or in the manufacture of a medicament for the above
 CC mentioned purposes. The epitopes are useful for diagnosing and treating
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
 CC diseases, cardiovascular diseases such as myocardial infarction,
 CC retinopathic diseases and other diseases mediated by abnormal platelet
 CC function and diseases caused by sulphated tyrosine-dependent protein-
 CC protein interactions. This sequence represents a human epitope sequence
 CC of the invention
 CC
 CC

SQ Sequence 13 AA;

Query Match 100.0%; Score 44; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.74;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YDYYPEE 7
 |||||
 Db 4 YDYYPEE 10

RESULT 4

ABG92029
 ID ABG92029 standard; peptide; 13 AA.

AC ABG92029;

DT 04-DEC-2002 (first entry)

DE Human epitope sequence #3.

XX Human; epitope; cancer; tumour; cell rolling; inflammation; metastasis;

XX hypervariable region; autoimmune disease; thrombosis; restenosis;

KM leukemia; inflammatory disease; cardiovascular disease;

KM myocardial infarction; retinopathic disease; abnormal platelet function;

KM sulphated tyrosine-dependent protein-protein interaction.

XX Homo sapiens.

PN WO200253700-A2.

PD 11-JUL-2002.

PF 31-DEC-2001; 2001WO-US049442.

PR 29-DEC-2000; 2000US-00751181.

PR 29-DEC-2000; 2000US-0258948P.

PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX Lazarevits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;

PI Sanchon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;

DR WPI; 2002-674776/72.

PT Novel isolated epitope present on cancer cells and important in

PT physiological phenomena such as cell rolling, metastasis and

PT inflammation, for treating autoimmune, inflammatory or cardiovascular

PT diseases, and cancer.

PS Claim 41; Page 132; ODP; English.

XX The invention relates to an isolated epitope present on cancer cells and

CC important in physiological phenomena such as cell rolling, metastasis and

CC inflammation, where the epitope is capable of being bound by an antibody,

CC its antigen-binding fragment or its complex comprising at least one

CC antibody or its binding fragment having a first hypervariable region. The

CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune

CC disease, thrombosis, restenosis, metastasis, growth and/or replication of

CC tumour or leukemia cells, increase in number of tumour or leukemia

CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-

CC platelet and/or cell-platelet adhesion or aggregation, for increasing

CC mortality of tumour or leukemia cells, for increasing the susceptibility

CC of diseased cells to damage by anti-disease, anti-cancer or anti-

CC leukemia agents, or for decreasing the number of tumour or leukemia

CC cells in a patient, or in the manufacture of a medicament for the above

CC mentioned purposes. The epitopes are useful for diagnosing and treating

CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory

CC diseases, cardiovascular diseases such as myocardial infarction,

CC retinopathic diseases and other diseases mediated by abnormal platelet

CC function and diseases caused by sulphated tyrosine-dependent protein-

CC protein interactions. This sequence represents a human epitope sequence

CC of the invention

XX Sequence 13 AA;

XX Query Match 100.0%; Score 44; DB 5; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.74;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YDYYPEE 7
 |||||
 Db 4 YDYYPEE 10

RESULT 5

ADJ57380
 ID ADJ57380 standard; peptide; 13 AA.

XX ADJ57380;

DT 06-MAY-2004 (first entry)

DE Human glycoprotein GP1b-alpha peptide.

XX GP1b-alpha; antibody; scFv; cytostatic; antiinflammatory;

KM immunosuppressive; human.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-size 5 /note="Sulfated"

PN WO2004003166-A2.

PD 08-JAN-2004.

PR 30-JUN-2003; 2003WO-US020602.

PR 01-JUL-2002; 2002US-00189032.

PA (SAVI-) SAVIENT PHARM INC.

XX Levanon A, Ben-Levy R, Plaksin D, Sanchon E, Hagai Y;

PI Hoch Mar-Chaim H;

DR WPI; 2004-203378/19.

PT Novel antibody or its fragment that binds to an epitope of P-selectin-

PT glycoprotein ligand-1, useful for diagnosing/prognosing inflammation,

PT infection, auto-immune disease, metastasis, tumor/leukemia cell in

PT patient.

PS Example 8; Page 56; 106pp; English.

XX The present sequence is that of a peptide sequence from human

CC glycoprotein GP1b-alpha. The peptide is sulfated at the Tyr residue at

CC position 4 of the sequence. It was one of a set of sulfated and non-

CC sulfated peptides used in an example from the invention to determine the

CC epitope for scFv antibody I32 ADJ57380. The results showed that the I32

CC epitope is located between amino acids 1 and 17 of mature P-selectin

CC glycoprotein ligand-1 (PSGL-1) in which there is a cluster of negatively

CC charged amino acids. The invention provides antibodies or their fragments

CC that have the binding specificity of I32. These are useful in

CC therapeutic, diagnostic, prognostic or staging methods for diseases such

CC as cancer, including tumour growth and metastasis, leukaemia, autoimmune

CC disease and inflammatory disease.

XX Sequence 13 AA;

XX Query Match 100.0%; Score 44; DB 8; Length 13;

XX Best Local Similarity 100.0%; Pred. No. 0.74;

XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 YDYYPEE 7

XX |||||

XX Db 4 YDYYPEE 10

```

RESULT 6
AAR38578
ID AAR38578 standard; peptide; 14 AA.
XX
AC AAR38578;
XX
DT 25-MAR-2003 (revised)
DT 05-NOV-1993 (first entry)
XX
DE GPIb-alpha-derived polypeptide subfragment 269-282.
XX
XX platelet; glycoprotein Ib-alpha; GPIb-alpha; von Willebrand factor;
XX bifunctional antithrombotic molecule; inhibition; activation; vWF;
XX adhesion; vascular surface; thrombin; thrombosis; endothelial cells;
XX fibroblasts; smooth muscle cells.
XX
OS Synthetic.
XX
PN WO9311778-A1.
XX
PD 24-JUN-1993.
XX
PF 11-DEC-1992; 92WO-US010947.
XX
PR 12-DEC-1991; 91US-00806709.
XX
PA (SCRI ) SCRIPPS RES INST.
XX
PI Ruggeri ZM, Ware JL, De Marco L, Mazzuato M;
XX WPI; 1993-213811/26.
XX
PT Bifunctional antithrombotic molecule and antithrombotic polypeptide - are
PT used to inhibit thrombosis, cell activation and tumor metastasis.
XX
PS Disclosure; Fig 1; 107pp; English.
XX
XX The sequences given in AAR38574-82 represents polypeptide fragments
CC derived from platelet glycoprotein Ib-alpha (GPIb-alpha). Sub-fragments
CC such as these may be used in the construction of a bifunctional
CC antithrombotic molecule. The bifunctional molecule inhibits activation
CC and/or adhesion of platelets to a damaged or diseased vascular surface.
CC The molecule contains two linked domains, the first inhibits binding of
CC thrombin to GPIb-alpha, and the other inhibiting binding of von
CC Willebrand factor (vWF) to GPIb-alpha. The molecule may be used to
CC inhibit thrombosis and cell activation of endothelial cells, fibroblasts
CC or smooth muscle cells. (Updated on 25-MAR-2003 to correct PN field.)
CC
SQ Sequence 14 AA;
XX
Query Match 100.0%; Score 44; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 YDYYPEB 7
DB 8 YDYYPEB 14
XX
RESULT 7
AAR13137
ID AAR13137 standard; peptide; 15 AA.
XX
AC AAR13137;
XX
XX
XX 25-MAR-2003 (revised)
XX 01-OCT-1991 (first entry)
XX
XX GPIb alpha peptide fragment.
XX
XX Von Willebrand factor; vWF; platelet membrane glycoprotein Ib;
XX glyocalicin; thrombosis.
XX

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```

OS Synthetic.
XX
PN WO9109614-A.
XX
PD 11-JUL-1991.
XX
PF 04-JAN-1990; 90US-00460674.
XX
PR 04-JAN-1990; 90US-00460674.
PR 14-NOV-1990; 90US-00613083.
XX
XX (SCRI ) SCRIPPS CLINIC & RES FOUND.
XX
XX Ruggeri ZM, Zimmerman TS, Houghten RA, Vicente V, Mohri H;
XX Ware JL;
XX WPI; 1991-222654/30.
XX
XX GPIb alpha peptide fragment - inhibits binding of von Willebrand factor
PT to platelet membrane glyco-protein Ib, useful in treating thrombosis.
XX
PS Claim 32; Page 59; 76pp; English.
XX
XX The peptide corresponds to residues 271-285 of the N-terminus of
CC glyocalicin, a water sol. proteolytic fragment of GPIb alpha. It may be
CC linked to a second peptide from the 45 kD N-terminal tryptic fragment of
CC GPIb alpha. The peptide inhibits binding of vWF to GPIb. It can be used
CC to inhibit activation, aggregation and/or adhesion of platelets, esp. for
CC inhibition of thrombosis. Truncated versions of the peptide may also be
CC used, esp. AAs 281-285. See also AAR13128-R13138. (Updated on 25-MAR-2003
XX to correct PA field.)
XX
SQ Sequence 15 AA;
XX
Query Match 100.0%; Score 44; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 YDYYPEB 7
DB 6 YDYYPEB 12
XX
RESULT 8
AAR38577
ID AAR38577 standard; peptide; 15 AA.
XX
AC AAR38577;
XX
XX
XX 25-MAR-2003 (revised)
XX 05-NOV-1993 (first entry)
XX
XX GPIb-alpha-derived polypeptide subfragment 271-285.
XX
XX platelet; glycoprotein Ib-alpha; GPIb-alpha; von Willebrand factor;
XX bifunctional antithrombotic molecule; inhibition; activation; vWF;
XX adhesion; vascular surface; thrombin; thrombosis; endothelial cells;
XX fibroblasts; smooth muscle cells.
XX
OS Synthetic.
XX
PN WO9311778-A1.
XX
PD 24-JUN-1993.
XX
PF 11-DEC-1992; 92WO-US010947.
XX
PR 12-DEC-1991; 91US-00806709.
XX
PA (SCRI ) SCRIPPS RES INST.
XX
XX Ruggeri ZM, Ware JL, De Marco L, Mazzuato M;
XX

```

DR WPI; 1993-213811/26.
 XX Bifunctional antithrombotic molecule and antithrombotic polypeptide - are
 PT used to inhibit thrombosis, cell activation and tumour metastasis.
 XX
 PS Disclosure; Fig 1; 107pp; English.
 XX
 CC The sequence given in AAR38574-82 represents polypeptide fragments
 CC derived from platelet glycoprotein Ib-alpha (GP1b-alpha). Sub-fragments
 CC such as these may be used in the construction of a bifunctional
 CC antithrombotic molecule. The bifunctional molecule inhibits activation
 CC and/or adhesion of platelets to a damaged or diseased vascular surface.
 CC The molecule contains two linked domains, the first inhibits binding of
 CC thrombin to GP1b-alpha, and the other inhibiting binding of von
 CC Willebrand factor (vWF) to GP1b-alpha. The molecule may be used to
 CC inhibit thrombosis and cell activation of endothelial cells, fibroblasts
 CC or smooth muscle cells. (Updated on 25-MAR-2003 to correct FN field.)
 CC
 SQ Sequence 15 AA;
 Query Match 100.0%; Score 44; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.86;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YDYYPEE 7
 |||||
 Db 6 YDYYPEE 12
 RESULT 9
 ID AAM14606 standard; peptide; 16 AA.
 XX AAM14606;
 AC
 DT 09-DEC-1997 (first entry)
 XX
 DE Human antithrombin III carboxy-terminal extension.
 XX
 KW Human; antithrombin III; mutant; carboxy-terminal; extension;
 KW sulphated tyrosine; prevention; treatment; thrombosis; disease.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 1..3
 FT /note= "carboxy-terminus of wild type human antithrombin
 FT III"
 XX
 PN JP09071600-A.
 XX
 XX 18-MAR-1997.
 PD
 XX 06-SEP-1995; 95JP-00228694.
 PF
 XX 06-SEP-1995; 95JP-00228694.
 PR
 XX (EISA) EISAI CO LTD.
 PA
 XX WPI; 1997-231188/21.
 DR
 XX Human antithrombin III mutant with C-terminal peptide containing a
 PT sulphated tyrosine - useful for treatment and prevention of thrombotic
 PT disease.
 PT
 XX Disclosure; Page 6; 11pp; Japanese.
 PS
 XX A human antithrombin III (AT III) mutant, comprising a carboxy-terminal
 CC sulphated tyrosine peptide extension, i.e. the present peptide, can be
 CC used to prevent and/or treat thrombotic diseases
 CC
 XX Sequence 16 AA;
 SQ

Query Match 100.0%; Score 44; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.92;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YDYYPEE 7
 |||||
 Db 7 YDYYPEE 13
 RESULT 10
 ID ABG92048 standard; peptide; 18 AA.
 ABG92048
 XX ABG92048
 AC ABG92048;
 DT 04-DEC-2002 (first entry)
 XX
 DE Human epitope sequence #21.
 XX
 KW Human; epitope; cancer; tumour; cell rolling; inflammation; metastasis;
 KW hypervariable region; autoimmune disease; thrombosis; restenosis;
 KW leukaemia; inflammatory disease; cardiovascular disease;
 KW myocardial infarction; retinopathic disease; abnormal platelet function;
 KW sulphated tyrosine-dependent protein-protein interaction.
 XX
 OS Homo sapiens.
 XX
 PN WO200253700-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 31-DEC-2001; 2001MO-US049442.
 XX
 XX 29-DEC-2000; 2000US-00751181.
 PR
 XX 29-DEC-2000; 2000US-0258948P.
 XX
 PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
 XX
 XX Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H,
 PT Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
 PT WPI; 2002-674776/72.
 DR
 XX Novel isolated epitope present on cancer cells and important in
 PT physiological phenomena such as cell rolling, metastasis and
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular
 PT diseases, and cancer.
 XX
 PS Disclosure; Page 60; 0pp; English.
 XX
 CC The invention relates to an isolated epitope present on cancer cells and
 CC important in physiological phenomena such as cell rolling, metastasis and
 CC inflammation, where the epitope is capable of being bound by an antibody,
 CC its antigen-binding fragment or its complex comprising at least one
 CC antibody or its binding fragment having a first hypervariable region. The
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing
 CC mortality of tumour or leukaemia cells, for increasing the susceptibility
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-
 CC leukaemia agents, or for decreasing the number of tumour or leukaemia
 CC cells in a patient, or in the manufacture of a medicament for the above
 CC mentioned purposes. The epitopes are useful for diagnosing and treating
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
 CC diseases, cardiovascular diseases such as myocardial infarction,
 CC retinopathic diseases and other diseases mediated by abnormal platelet
 CC function and diseases caused by sulphated tyrosine-dependent protein-
 CC protein interactions. This sequence represents a human epitope sequence
 CC of the invention
 XX
 XX Sequence 18 AA;
 SQ

Query Match 100.0%; Score 44; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YDYPER 7
|||||
9 YDYPER 15

DB 9 YDYPER 15

RESULT 11
ABG92049
ID ABG92049 standard; peptide, 18 AA.
XX
AC ABG92049;
XX
DT 04-DEC-2002 (first entry)
XX
DE Human epitope sequence #22.
XX
KW Human; epitope; cancer; tumour; cell rolling; inflammation; metastasis;
KW hypervariable region; autoimmune disease; thrombosis; restenosis;
KW leukemia; inflammatory disease; cardiovascular disease;
KW myocardial infarction; retinopathic disease; abnormal platelet function;
KW sulphated tyrosine-dependent protein-protein interaction.
XX
OS Homo sapiens.
XX
PN WO200253700-A2.
XX
PD 11-JUL-2002.
XX
PF 31-DEC-2001; 2001WO-US049442.
XX
PR 29-DEC-2000; 2000US-00751181.
PR 29-DEC-2000; 2000US-0258948P.
XX
PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX
PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H,
PI Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
DR WPI; 2002-674776/72.
XX
PT Novel isolated epitope present on cancer cells and important in
PT physiological phenomena such as cell rolling, metastasis and
PT inflammation, for treating autoimmune, inflammatory or cardiovascular
PT diseases, and cancer.
XX
PS Disclosure; Page 60; 0pp; English.
XX
CC The invention relates to an isolated epitope present on cancer cells and
CC important in physiological phenomena such as cell rolling, metastasis and
CC inflammation, where the epitope is capable of being bound by an antibody,
CC its antigen-binding fragment or its complex comprising at least one
CC antibody or its binding fragment having a first hypervariable region. The
CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
CC tumour or leukemia cells, increase in number of tumour or leukemia
CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
CC platelet and/or cell-platelet adhesion or aggregation, for increasing
CC mortality of tumour or leukemia cells, for increasing the susceptibility
CC of diseased cells to damage by anti-disease, anti-cancer or anti-
CC leukemia agents, or for decreasing the number of tumour or leukemia
CC cells in a patient, or in the manufacture of a medicament for the above
CC mentioned purposes. The epitopes are useful for diagnosing and treating
CC diseases such as cancer, leukemia, autoimmune diseases, inflammatory
CC diseases, cardiovascular diseases such as myocardial infarction,
CC retinopathic diseases and other diseases mediated by abnormal platelet
CC function and diseases caused by sulphated tyrosine-dependent protein-
CC protein interactions. This sequence represents a human epitope sequence
CC of the invention
XX

SQ Sequence 18 AA;
Query Match 100.0%; Score 44; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YDYPER 7
|||||
9 YDYPER 15

DB 9 YDYPER 15

RESULT 12
ABG92057
ID ABG92057 standard; peptide, 18 AA.
XX
AC ABG92057;
XX
DT 04-DEC-2002 (first entry)
XX
DE Human epitope sequence #30.
XX
KW Human; epitope; cancer; tumour; cell rolling; inflammation; metastasis;
KW hypervariable region; autoimmune disease; thrombosis; restenosis;
KW leukemia; inflammatory disease; cardiovascular disease;
KW myocardial infarction; retinopathic disease; abnormal platelet function;
KW sulphated tyrosine-dependent protein-protein interaction.
XX
OS Homo sapiens.
XX
PN WO200253700-A2.
XX
PD 11-JUL-2002.
XX
PF 31-DEC-2001; 2001WO-US049442.
XX
PR 29-DEC-2000; 2000US-00751181.
PR 29-DEC-2000; 2000US-0258948P.
XX
PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX
PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H,
PI Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
DR WPI; 2002-674776/72.
XX
PT Novel isolated epitope present on cancer cells and important in
PT physiological phenomena such as cell rolling, metastasis and
PT inflammation, for treating autoimmune, inflammatory or cardiovascular
PT diseases, and cancer.
XX
PS Disclosure; Page 74; 0pp; English.
XX
CC The invention relates to an isolated epitope present on cancer cells and
CC important in physiological phenomena such as cell rolling, metastasis and
CC inflammation, where the epitope is capable of being bound by an antibody,
CC its antigen-binding fragment or its complex comprising at least one
CC antibody or its binding fragment having a first hypervariable region. The
CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
CC tumour or leukemia cells, increase in number of tumour or leukemia
CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
CC platelet and/or cell-platelet adhesion or aggregation, for increasing
CC mortality of tumour or leukemia cells, for increasing the susceptibility
CC of diseased cells to damage by anti-disease, anti-cancer or anti-
CC leukemia agents, or for decreasing the number of tumour or leukemia
CC cells in a patient, or in the manufacture of a medicament for the above
CC mentioned purposes. The epitopes are useful for diagnosing and treating
CC diseases such as cancer, leukemia, autoimmune diseases, inflammatory
CC diseases, cardiovascular diseases such as myocardial infarction,
CC retinopathic diseases and other diseases mediated by abnormal platelet
CC function and diseases caused by sulphated tyrosine-dependent protein-
CC protein interactions. This sequence represents a human epitope sequence
CC of the invention
XX

XX SO Sequence 18 AA; Query Match 100.0%; Score 44; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YDYYPEE 7
Db 9 YDYYPEE 15

RESULT 13
ADJ57379 standard; peptide; 18 AA.
XX ADJ57379;
XX 06-MAY-2004 (first entry)
XX Human glycoprotein GP1b-alpha peptide.
XX GP1b-alpha; antibody; scFv; cytostatic; antiinflammatory;
XX immunosuppressive; human.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Modified-site 9 /note= "Optionally sulfated"
FT Modified-site 11 /note= "Optionally sulfated"
FT Modified-site 12 /note= "Optionally sulfated"
FT Modified-site 12 /note= "Optionally sulfated"
XX W02004003166-A2.
XX 08-JAN-2004.
XX 30-JUN-2003; 2003WO-US020602.
XX 01-JUL-2002; 2002US-00189032.
XX (SAVR-) SAVIENT PHARM INC.
XX Levanon A, Ben-Levy R, Plaksin D, Szanton E, Hagai Y;
XX Hoch Mar- Chaim H;
XX WPI; 2004-203378/19.
XX Novel antibody or its fragment that binds to an epitope of P-selectin-
PT glycoprotein Ligand-1, useful for diagnosing/prognosing inflammation,
PT infection, auto-immune disease, metastasis, tumor/leukemia cell in
XX patient.
XX Example 8; Page 55; 106pp; English.
XX The present sequence is that of a peptide sequence from human
CC glycoprotein GP1b-alpha. The peptide may be non-sulfated or sulfated at
CC one or more of the Tyr residues at positions 9, 11 and 12 of the
CC sequence. These sulfated and non-sulfated peptides were used in an
CC example from the invention to determine the epitope for scFv antibody L32
CC ADJ57363. The results showed that the L32 epitope is located between
CC amino acids 1 and 17 of mature P-selectin glycoprotein ligand-1 (PSGL-1)
CC in which there is a cluster of negatively charged amino acids. The
CC invention provides antibodies or their fragments that have the binding
CC specificity of L32. These are useful in therapeutic, diagnostic,
CC prognostic or staging methods for diseases such as cancer, including
CC tumor growth and metastasis, leukaemia, autoimmune disease and
CC inflammatory disease.
XX Sequence 18 AA;

XX SO Query Match 100.0%; Score 44; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YDYYPEE 7
Db 9 YDYYPEE 15

RESULT 14
ABG92028 standard; peptide; 19 AA.
XX ABG92028;
XX 04-DEC-2002 (first entry)
XX Human epitope sequence #2.
XX Human; epitope; cancer; tumour; cell rolling; inflammation; metastasis;
XX hypervariable region; autoimmune disease; thrombosis; restenosis;
XX leukaemia; inflammatory disease; cardiovascular disease;
XX myocardial infarction; retinopathic disease; abnormal platelet function;
XX sulfated tyrosine-dependent protein-protein interaction.
XX Homo sapiens.
XX W0200253700-A2.
XX 11-JUL-2002.
XX 31-DEC-2001; 2001WO-US049442.
XX 29-DEC-2000; 2000US-00751181.
XX 29-DEC-2000; 2000US-0258948P.
XX (BIOR-) BIO-TECHNOLOGY GEN CORP.
XX Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
XX Szanton E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
XX WPI; 2002-674776/72.
XX Novel isolated epitope present on cancer cells and important in
PT physiological phenomena such as cell rolling, metastasis and
PT inflammation, for treating autoimmune, inflammatory or cardiovascular
PT diseases, and cancer.
XX Claim 40; Page 131; 0pp; English.
XX The invention relates to an isolated epitope present on cancer cells and
CC important in physiological phenomena such as cell rolling, metastasis and
CC inflammation, where the epitope is capable of being bound by an antibody,
CC its antigen-binding fragment or its complex comprising at least one
CC antibody or its binding fragment having a first hypervariable region. The
CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
CC tumour or leukaemia cells, increase in number of tumour or leukaemia
CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
CC platelet and/or cell-platelet adhesion or aggregation, for increasing
CC mortality of tumour or leukaemia cells, for increasing the susceptibility
CC of diseased cells to damage by anti-disease, anti-cancer or anti-
CC leukaemia agents, or for decreasing the number of tumour or leukaemia
CC cells in a patient, or in the manufacture of a medicament for the above
CC mentioned purposes. The epitopes are useful for diagnosing and treating
CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
CC diseases, cardiovascular diseases, such as myocardial infarction,
CC retinopathic diseases and other diseases mediated by abnormal platelet
CC function and diseases caused by sulfated tyrosine-dependent protein-
CC protein interactions. This sequence represents a human epitope sequence
XX of the invention
XX Sequence 19 AA;

Query Match 100.0%; Score 44; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YDYYPEE 7
| | | | |
| | | | |
Db 8 YDYYPEE 14

RESULT 15
ABG92052
ID ABG92052 standard; peptide; 19 AA.
XX
XX
AC ABG92052;
XX
DT 04-DEC-2002 (first entry)
XX
DE Human epitope sequence #25.
XX
XX Human; epitope; cancer; tumour; cell rolling; inflammation; metastasis;
KM hypervariable region; autoimmune disease; thrombosis; restenosis;
KM leukemia; inflammatory disease; cardiovascular disease;
KM myocardial infarction; retinopathic disease; abnormal platelet function;
KM sulphated tyrosine-dependent protein-protein interaction.
XX
OS Homo sapiens.
XX
XX
PN WO200253700-A2.
XX
PD 11-JUL-2002.
XX
PF 31-DEC-2001; 2001WO-US049442.
XX
PR 29-DEC-2000; 2000US-00751181.
XX 29-DEC-2000; 2000US-0258948P.
XX
XX
PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX
PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
PI Szanichon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
XX
XX MPI; 2002-674776/72.
XX
PT Novel isolated epitope present on cancer cells and important in
PT physiological phenomena such as cell rolling, metastasis and
PT inflammation, for treating autoimmune, inflammatory or cardiovascular
PT diseases, and cancer.
XX
PS Disclosure; Page 72; 0pp; English.
XX
XX The invention relates to an isolated epitope present on cancer cells and
CC important in physiological phenomena such as cell rolling, metastasis and
CC inflammation, where the epitope is capable of being bound by an antibody,
CC its antigen-binding fragment or its complex comprising at least one
CC antibody or its binding fragment having a first hypervariable region. The
CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
CC tumour or leukemia cells, increase in number of tumour or leukemia
CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
CC platelet and/or cell-platelet adhesion or aggregation, for increasing
CC mortality of tumour or leukemia cells, for increasing the susceptibility
CC of diseased cells to damage by anti-disease, anti-cancer or anti-
CC leukemia agents, or for decreasing the number of tumour or leukemia
CC cells in a patient, or in the manufacture of a medicament for the above
CC mentioned purposes. The epitopes are useful for diagnosing and treating
CC diseases such as cancer, leukemia, autoimmune diseases, inflammatory
CC diseases, cardiovascular diseases such as myocardial infarction,
CC retinopathic diseases and other diseases mediated by abnormal platelet
CC function and diseases caused by sulphated tyrosine-dependent protein-
CC protein interactions. This sequence represents a human epitope sequence
XX of the invention

SQ Sequence 19 AA;
Query Match 100.0%; Score 44; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YDYYPEE 7
| | | | |
| | | | |
Db 8 YDYYPEE 14

Search completed: September 9, 2005, 16:25:45
Job time : 108.45 secs

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OM protein - protein search, using sw model

Run on: September 9, 2005, 16:13:21 ; Search time 20.65 Seconds

(without alignments)
32.616 Million cell updates/sec

Title: US-10-032-037C-266

Perfect score: 44

Sequence: 1 YDYPPB 7

Scoring table: BLOSUM62

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

PIR 79:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	626	1 NBHUIA	platelet glycoprot
2	37	84.1	344	2 JC6100	CA2CC-box binding
3	37	84.1	547	2 F82162	paranet-inducible
4	37	84.1	802	2 F90060	copper-transferrin
5	37	84.1	803	2 JC7862	eukaryotic initiator
6	37	84.1	980	2 T00045	cellodextrin phosph
7	37	84.1	1805	2 T02712	similar to late em
8	36	81.8	364	2 H89973	conserved hypochet
9	36	81.8	956	1 P2XR10	major outer capsid
10	35	79.5	141	2 I50096	MHC class II beta
11	35	79.5	212	2 G90353	2-haloalkanoic aci
12	35	79.5	212	2 H90369	MHC class II beta
13	35	79.5	246	2 I50094	MHC class II beta
14	35	79.5	246	2 H70223	conserved hypochet
15	35	79.5	247	2 I50093	MHC class II beta
16	35	79.5	248	2 S35076	class II histocomp
17	35	79.5	290	2 T42526	hypothetical prote
18	35	79.5	343	2 G71499	probable D-Ala-D-A
19	35	79.5	370	1 A48252	neuropeptide allat
20	35	79.5	438	2 F81659	D-alanyl-D-alanine
21	35	79.5	1163	1 GNMVY8	genome polypeptid
22	35	79.5	1483	1 S30015	hypothetical prote
23	35	79.5	3411	1 GNMVY	genome polypeptid
24	35	79.5	3411	1 GNMVY	genome polypeptid
25	34	77.3	125	2 AB1651	hypothetical prote
26	34	77.3	135	2 A11588	hypothetical prote
27	34	77.3	139	2 H86800	hypothetical prote
28	34	77.3	139	2 D86753	hypothetical prote
29	34	77.3	139	2 G86681	hypothetical prote

30	34	77.3	180	2 AD1900	hypothetical prote
31	34	77.3	209	2 G71222	hypothetical prote
32	34	77.3	263	2 T19387	hypothetical prote
33	34	77.3	274	2 D84701	hypothetical prote
34	34	77.3	297	2 T25652	degenerin 1 (DEG-1
35	34	77.3	324	2 AH3548	glucuronate 2-dehydr
36	34	77.3	421	2 E69467	hypothetical prote
37	34	77.3	423	2 A12326	hypothetical prote
38	34	77.3	427	2 AF2014	hypothetical prote
39	34	77.3	431	2 A86776	histidinol dehydro
40	34	77.3	431	2 E45734	histidinol dehydro
41	34	77.3	465	2 T16618	hypothetical prote
42	34	77.3	672	2 E72391	beta-D-galactosida
43	34	77.3	676	2 S40939	hypothetical prote
44	34	77.3	961	1 P2XRSA	outer capsid prote
45	34	77.3	1380	2 T18309	receptor-adenylate

ALIGNMENTS

RESULT 1

platelet glycoprotein Ib alpha chain precursor - human
N/Alternate names: membrane glycoprotein Ib alpha chain
N/Contains: glycosylated
C/Species: Homo sapiens (man)
C/Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text change 09-Jul-2004
C/Accession: A94174; A60435; A94173; S16945; I55355; A27075; A27102
R/Lopez, J.A.; Chung, D.W.; Fujikawa, K.; Hagen, F.S.; Papayannopolou, T.; Roth, G.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 5615-5619, 1987
A/Title: Cloning of the alpha-chain of human platelet glycoprotein Ib: a transmembrane
A/Reference number: A94174; PMID:87289655; PMID:3303030
A/Accession: A94174
A/Molecule type: mRNA
A/Residues: 1-626 <LOP>
A/Cross-references: UNIPROT:P07359; GB:J02940; NID:g183499; PIND:AAA52595.1; PID:g30679
R/Wick, A.N.; Walz, A.; Gerber-Huber, S.N.; Wenger, R.H.; Vornhagen, R.; Clemenson, K.
Thromb. Haemost. 61, 448-453, 1989
A/Title: Isolation and characterization of human blood platelet mRNA and construction of
d cloning of a GPIb coding cDNA insert.
A/Reference number: A60435; PMID:90020160; PMID:2799758
A/Accession: A60435
A/Molecule type: mRNA
A/Residues: 207-467 <WIC>
R/Titani, K.; Takio, K.; Handa, M.; Ruggeri, Z.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 5610-5614, 1987
A/Title: Amino acid sequence of the von Willebrand factor-binding domain of platelet mem
A/Reference number: A94173; PMID:87289654; PMID:3497398
A/Accession: A94173
A/Molecule type: protein
A/Residues: 17-315 <TIR>
R/Hess, D.; Schaller, J.; Rickli, E.E.; Clemenson, K.J.
Eur. J. Biochem. 199, 389-393, 1991
A/Title: Identification of the disulphide bonds in human platelet glycosylated.
A/Reference number: S16945; PMID:91301149; PMID:2070794
A/Accession: S16945
A/Status: preliminary
A/Molecule type: protein
A/Residues: 224-227;262-270;277-282 <HRS>
R/Lopez, J.A.; Ludwig, E.H.; McCarthy, B.J.
U. Biol. Chem. 267, 10055-10061, 1992
A/Title: Polymorphism of human glycoprotein Ib alpha results from a variable number of r
actions.
A/Reference number: I55355; PMID:92250564; PMID:1577776
A/Accession: I55355
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 412-427 <RBS>
A/Cross-references: GB:S34436; NID:g249176; PIND:AA822152.1; PID:g249177
A/Note: variant D
C/Comment: Glycoprotein Ib (GPIb), a surface membrane protein of platelets, participates
C/Comment: Platelet activation apparently involves disruption of the macromolecular comp

C/Comment: Binding sites for von Willebrand factor and thrombin (the latter site with un
C/Comment: Glycocallectin, which is approximately coextensive with the extracellular part
C/Genetics:
A:Gene: GDB:GP1BA, GP1B
A:Cross-references: GDB:118806; OMIM:231200
A:Map position: 17pter-17p12
C/Complex: heterodimer with platelet glycoprotein Ib beta chain (NBHUIB)
C/Superfamily: platelet glycoprotein Ib alpha chain; leucine-rich alpha-2-glycoprotein x
C/Keywords: blood coagulation; duplication; glycoprotein; platelet membrane; tandem repe
F/1-16/Domain: signal sequence #status predicted <SIG>
F/17-626/Product: platelet glycoprotein Ib alpha chain #status predicted <MP>
F/8-71/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR1>
F/12-91/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>
F/94-116/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
F/117-140/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>
F/141-164/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>
F/165-188/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>
F/189-212/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>
F/379-430/Region: proline/threonine-rich 9-residue repeats
F/502-540/Domain: transmembrane #status predicted <TM>
F/541-626/Domain: intracellular #status predicted <INT>
F/37.175/Binding site: carbohydrate (Thr) (covalent) #status experimental
F/308/Binding site: carbohydrate (Thr) (covalent) #status experimental

Query Match 100.0%; Score 44; DB 1; Length 626;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYPPER 7
Db 292 DYPPER 298

RESULT 2

JC6100
CACCC-box binding protein BKLf - mouse
C/Species: Mus musculus (house mouse)
C/Date: 13-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C/Accession: JC6100
R:Crossley, M.; Whitelaw, B.; Perkins, A.; Williams, G.; Fujiwara, Y.; Okkin, S.H.
Mol. Cell. Biol. 16, 1695-1705, 1996
A/Title: Isolation and characterization of the cDNA encoding BKLf/TFE-2, a major CACCC-B
A/Reference number: JC6100; MUID:96239526; PMID:8657145
A/Accession: JC6100
A:Molecule type: mRNA
A:Residues: 1-344 <CRO>
A:Cross-references: UNIPROT:Q60980; GB:U36340; NID:g1244514; PIDN:AAA93256.1; PID:g12445
A/Experimental source: erythroid cell
C/Comment: This protein is a member of the Krueppel family of transcription factors. It
C/Keywords: transcription factor; zinc finger

Query Match 84.1%; Score 37; DB 2; Length 344;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYPPER 7
Db 208 DYPPER 213

RESULT 3

PARACUAT-inducible protein B VC1754 [imported] - Vibrio cholerae (strain N16961 serogrou
C/Species: Vibrio cholerae
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C/Accession: F82162
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
Chardon, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A/Reference number: A82035; MUID:20406833; PMID:10952301
A/Accession: F82162

A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-547 <HEI>
A:Cross-references: UNIPROT:Q9KX88; GB:AE004252; GB:AE003852; NID:g9656263; PIDN:AAF9490
A/Experimental source: serogroup O1, strain N16961; biotype El Tor
C/Genetics:
A:Gene: VC1754
A:Map position: 1
C/Superfamily: pgiB protein

Query Match 84.1%; Score 37; DB 2; Length 547;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYPPER 7
Db 395 DYPPER 400

RESULT 4

F90060
copper-transporting ATPase copA [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: F90060
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratsugu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; MUID:2111952; PMID:11418146
A/Accession: F90060
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-802 <KUN>
A:Cross-references: UNIPROT:Q99880; GB:BA000018; PID:g13702507; PIDN:BA843648.1; GSPDB:G
A/Experimental source: strain N315
C/Genetics:
A:Gene: copA
C/Superfamily: Bacillus probable copper-transporting ATPase ywX; ATPase nucleotide-bind

Query Match 84.1%; Score 37; DB 2; Length 802;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYPPER 7
Db 115 DYPPER 120

RESULT 5

JC7862
eukaryotic initiation factor eIF3 subunit, p16 protein - mouse
C/Species: Mus musculus (house mouse)
C/Date: 18-Nov-2002 #sequence_revision 18-Nov-2002 #text_change 09-Jul-2004
C/Accession: JC7862
R:Koyanagi-Katsuta, R.; Akimitsu, N.; Hamamoto, H.; Arimitsu, N.; Hatano, T.; Sekimizu,
J. Biochem. 131, 833-837, 2002
A/Title: Embryonic lethality of mutant mice deficient in the p16 gene.
A/Reference number: JC7862; MUID:22035555; PMID:12038979
A/Accession: JC7862
A:Molecule type: mRNA
A:Residues: 1-803 <KOY>
A:Cross-references: UNIPROT:Q8JZQ9
C/Comment: This protein, a subunit of the eukaryotic translation initiation eIF3, having
of mouse development.
C/Genetics:
A:Gene: p16
C/Superfamily: translation initiation factor eIF-3b

Query Match 84.1%; Score 37; DB 2; Length 803;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DYPPEE 7
|||||
Db 209 DYPPEE 214

RESULT 6

T00045
cellohextrin phosphorylase - Clostridium thermocellum
C/Species: Clostridium thermocellum
C/Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
C/Accession: T00045
R/Kawaguchi, T.; Ikeuchi, Y.; Tetsunari, N.; Kan, A.; Sumitani, J.; Arai, M.
J. Ferment. Bioeng. 85, 144-149, 1998
A/Title: Cloning, nucleotide sequence, and expression of the Clostridium thermocellum ce
A/Reference number: 214077
A/Accession: T00045
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-980 <KAM>
A/Cross-references: UNIPROT:Q24780; EMBL:AB006822; NID:d1117395; PIDN:BA42081.1; PID:dl
A/Experimental source: ATCC 27405
C/Genetics:
A/Gene: cdp

Query Match 84.1%; Score 37; DB 2; Length 980;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DYPPEE 7
|||||
Db 323 DYPPEE 328

RESULT 7

T02712
similar to late embryogenesis abundant proteins [imported] - Arabidopsis thaliana
N/Alternate names: hypochemical protein T18E12.19
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C/Accession: T02712; G84444
R/Rounsailey, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.; Shen, M.; Ror
submitted to the EMBL Data Library, September 1998
A/Description: Arabidopsis thaliana chromosome II BAC T18E12 genomic sequence.
A/Reference number: 214702
A/Accession: T02712
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1805 <ROU>
A/Cross-references: UNIPROT:O81060; EMBL:AC005313; NID:g3548797; PID:g3548816
A/Experimental source: cultivar Columbia
R/Lin, X.; Kaul, S.; Rounsailey, S.D.; Shea, T.P.; Bentto, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.
eues, D.; Nierman, W.C.; White, O.; Eissen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: A84420; MUID:20083487; PMID:10617197
A/Accession: G84444
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1805 <STO>
A/Cross-references: GB:AE002093; NID:g3548816; PIDN:AAAC34488.1; GSPDB:GN00139
C/Genetics:
A/Gene: T18E12.19; AC2903140
A/Map position: 2
A/Intons: 249/2; 341/3; 403/3; 451/1; 611/3; 1414/3; 1471/2; 1523/2; 1603/3; 1707/2

Query Match 84.1%; Score 37; DB 2; Length 1805;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DYPPEE 7
|||||

Db 1112 DYPPEE 1117

RESULT 8

H89973
conserved hypothetical protein SA1682 [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: H89973
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu
ma, A.; Mizutani, U.; Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; MUID:21311952; PMID:11418146
A/Accession: H89973
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-364 <KUR>
A/Cross-references: UNIPROT:Q99T14; GB:BA000018; PID:g13701658; PIDN:BA842951.1; GSPDB:
A/Experimental source: strain N315
C/Genetics:
A/Gene: SA1682

Query Match 81.8%; Score 36; DB 2; Length 364;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YDYPPEE 7
|||||
Db 199 YDYPPEE 205

RESULT 9

P2XR10
major outer capsid protein VP2 - bluetongue virus (serotype 10, American isolate)
N/Alternate names: BTV hemagglutinin protein; principal serotype-determining antigen
C/Species: bluetongue virus
C/Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C/Accession: A25484; S10535
R/Purdy, M.A.; Ghiasi, H.; Rao, C.D.; Roy, P.
J. Virol. 55, 826-830, 1985
A/Title: Complete sequence of bluetongue virus 12 RNA that codes for the antigen recogni
A/Reference number: A25484; MUID:85265048; PMID:2991598
A/Accession: A25484
A/Molecule type: genomic RNA
A/Residues: 1-956 <PUR>
A/Cross-references: UNIPROT:P06945; GB:M11787; GB:M16566; NID:g210854; PIDN:AAA42828.1;
R/Roy, P.; Marshall, J.J.A.; French, T.J.
Curr. Top. Microbiol. Immunol. 162, 43-87, 1990
A/Title: Structure of the bluetongue virus genome and its encoded proteins.
A/Reference number: S10534; MUID:90345726; PMID:2166648
A/Accession: S10535
A/Status: preliminary
A/Molecule type: genomic RNA
A/Residues: 1-956 <ROY>
C/Genetics:
A/Map position: segment 2
C/Superfamily: bluetongue virus VP2 protein
C/Keywords: capsid protein; hemagglutinin

Query Match 81.8%; Score 36; DB 1; Length 956;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YDYPPEE 7
|||||
Db 149 YDYPPEE 155

RESULT 10

150096
MHC class II beta chain - Aulonocara hanabanechi (fragment)

C/Species: Aulonocara hansbaenschi
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C/Accession: I50096
R/Ono, H.; O'huglin, C.; Vincek, V.; Klein, J.
Immunogenetics 38, 223-234, 1993
A/Title: Exon-intron organization of fish major histocompatibility complex class II B gene
A/Reference number: I50093; MUID:93279741; PMID:8505065
A/Accession: I50096
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1141 <ON>
A/Cross-references: UNIPROT:Q08612; GB:U13229; NID:g289228; PIDN:AAA48549.1; PID:g555415
C/Genetics:
A/Intons: 91/1
C/Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 79.5%; Score 35; DB 2; Length 141;
Best Local Similarity 71.4%; Pred. No. 29;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YDYYPE 7
||:||||
Db 116 YDYYPE 122

RESULT 11
G90353
2-haloalkanoic acid dehalogenase [imported] - Sulfolobus solfataricus
C/Species: Sulfolobus solfataricus
C/Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C/Accession: G90353
R/She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aways, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.
arrett, R.A.; Ragan, M.A.; Sersen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A/Description: Sulfolobus solfataricus complete genome.
A/Reference number: A99139
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-212 <NR>
A/Cross-references: UNIPROT:Q97X58; GB:AE006641; NID:g13815156; PIDN:AAK42086.1; GSPDB:G
C/Genetics:
A/Gene: SSO1896

Query Match 79.5%; Score 35; DB 2; Length 212;
Best Local Similarity 83.3%; Pred. No. 45;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YDYYPE 6
||:||||
Db 188 YDYYPE 193

RESULT 12
H90369
2-haloalkanoic acid dehalogenase [imported] - Sulfolobus solfataricus
C/Species: Sulfolobus solfataricus
C/Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C/Accession: H90369
R/She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aways, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.
arrett, R.A.; Ragan, M.A.; Sersen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A/Description: Sulfolobus solfataricus complete genome.
A/Reference number: A99139
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-212 <NR>
A/Cross-references: UNIPROT:Q97W76; GB:AE006641; NID:g138151509; PIDN:AAK4215.1; GSPDB:G
C/Genetics:
A/Gene: SSO2028

Query Match 79.5%; Score 35; DB 2; Length 212;
Best Local Similarity 83.3%; Pred. No. 45;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YDYYPE 6
||:||||
Db 188 YDYYPE 193

RESULT 13
I50094
MHC class II beta chain - Aulonocara hansbaenschi (fragment)
C/Species: Aulonocara hansbaenschi
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C/Accession: I50094
R/Ono, H.; O'huglin, C.; Vincek, V.; Klein, J.
Immunogenetics 38, 223-234, 1993
A/Title: Exon-intron organization of fish major histocompatibility complex class II B gene
A/Reference number: I50093; MUID:93279741; PMID:8505065
A/Accession: I50094
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-246 <ON>
A/Cross-references: UNIPROT:Q08608; GB:U13223; NID:g289224; PIDN:AAA48547.1; PID:g289225
F:122-187/Domain: immunoglobulin homology <IM>

Query Match 79.5%; Score 35; DB 2; Length 246;
Best Local Similarity 71.4%; Pred. No. 52;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YDYYPE 7
||:||||
Db 132 YDYYPE 138

RESULT 14
H70223
conserved hypothetical protein BBD21 - Lyme disease spirochete plasmid D/1p17
C/Species: Borrelia burgdorferi (Lyme disease spirochete)
C/Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C/Accession: H70223
R/Frazer, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White-
son, D.; Peterson, J.; Kervatage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A/Authors: Smith, H.O.; Venter, J.C.
A/Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.
A/Reference number: A70100; MUID:98065943; PMID:9403685
A/Accession: H70223
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-246 <KLE>
A/Cross-references: UNIPROT:P70843; GB:AE000793; NID:g2689927; PIDN:AAc66345.1; PID:g268
A/Experimental source: strain B31
C/Genetics:
A/Genome: plasmid
C/Superfamily: Lyme disease spirochete plasmid probable stage 0 sporulation protein J

Query Match 79.5%; Score 35; DB 2; Length 246;
Best Local Similarity 83.3%; Pred. No. 52;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YDYYPE 6
||:||||
Db 225 YDYYPE 230

RESULT 15
I50093
MHC class II beta chain - Aulonocara hansbaenschi (fragment)
C/Species: Aulonocara hansbaenschi

C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
 C/Accession: I50093
 R/Ono, H.; O'hUigin, C.; Vincek, V.; Klein, J.
 Immunogenetics 38, 223-234, 1993
 A>Title: Exon-intron organization of fish major histocompatibility complex class II B gene
 A/Reference number: I50093; MUID:93279741; PMID:8505065
 A/Accession: I50093
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-247 <ONO>
 A/Cross-references: UNIPROT:Q08606; GB:LI13222; NID:G289221; PIDN:AAA48546.1; PID:G289222
 C/Superfamily: class II histocompatibility antigen; immunoglobulin homology
 F:123-188/Domain: immunoglobulin homology <IMM>

Query Match 79.5%; Score 35; DB 2; Length 247;
 Best Local Similarity 71.4%; Pred. NO. 52;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YDYYPPEE 7
 |||||
 Db 133 YDYYPPEE 139

Search completed: September 9, 2005, 16:31:45
 Job time : 22.65 secs

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OM protein - protein search, using sw model

Run on: September 9, 2005, 15:58:05 ; Search time 100.1 Seconds
(without alignments)
35.810 Million cell updates/sec

Title: US-10-032-037C-266

Perfect score: 44

Sequence: 1 YDYYPE 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	626	1	GPBA_HUMAN
2	40	90.9	945	1	G742A0
3	38	86.4	493	1	OCLN_XENTLA
4	37	84.1	161	2	Q9KWC7
5	37	84.1	232	2	Q86TNO
6	37	84.1	274	2	Q8BV07
7	37	84.1	301	2	Q8PXU9
8	37	84.1	305	2	Q9HHP9
9	37	84.1	344	1	KLFP_MOUSE
10	37	84.1	345	1	KLFP_HUMAN
11	37	84.1	345	2	Q6PIR1
12	37	84.1	431	2	Q6L308
13	37	84.1	441	2	Q962Y5
14	37	84.1	468	2	Q8A2A4
15	37	84.1	547	2	Q9KX88
16	37	84.1	560	2	Q97AH8
17	37	84.1	641	2	Q922K2
18	37	84.1	749	1	APB2_HUMAN
19	37	84.1	802	2	Q8N0Q9
20	37	84.1	802	2	Q99R80
21	37	84.1	802	2	Q7A3B6
22	37	84.1	802	2	Q6G6B7
23	37	84.1	802	2	Q6GDP1
24	37	84.1	803	2	Q8JZQ9
25	37	84.1	970	2	Q8CJ33
26	37	84.1	980	2	Q24780
27	37	84.1	984	2	Q93HT8
28	37	84.1	1805	2	Q81060
29	36	81.8	297	2	Q8IMK6
30	36	81.8	297	2	Q8MZB6
31	36	81.8	308	2	Q9ZAY0

32	36	81.8	336	2	Q9VA15	Q9VA15 drosophila
33	36	81.8	349	1	RNPD_BUCAP	Q8KA19 buchnera ap
34	36	81.8	364	2	Q99T14	Q99T14 staphylococ
35	36	81.8	364	2	Q7A0J2	Q7A0J2 staphylococ
36	36	81.8	364	2	Q7A4T4	Q7A4T4 staphylococ
37	36	81.8	364	2	Q6G869	Q6G869 staphylococ
38	36	81.8	364	2	Q6G6J2	Q6G6J2 staphylococ
39	36	81.8	365	2	Q9VZ54	Q9VZ54 drosophila
40	36	81.8	413	2	Q7S2S2	Q7S2S2 neuropept
41	36	81.8	690	2	Q7RT71	Q7RT71 plasmodium
42	36	81.8	811	2	Q7Q6P4	Q7Q6P4 anopheles g
43	36	81.8	882	1	SYA_SYNE1	Q8DH56 synchococc
44	36	81.8	956	1	VP2_BTIV10	Q69345 bluetongue
45	36	81.8	956	2	Q65735	Q65735 bluetongue

ALIGNMENTS

RESULT 1

GPBA_HUMAN STANDARD; PRT; 626 AA.

AC P07359; Q14441; Q16469; Q8N1F3; Q8NG39; Q9HDC7; Q9UEK1; Q9UQ54;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DE 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Platelet glycoprotein Ib alpha chain precursor (Glycoprotein Ibalph)
 DE (GP-Ib alpha) (GP1BA) (GP1B-alpha) (CD42B-alpha) [Contains:
 DE glycosylated].
 GN Name=GP1BA;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RX MEDLINE=87289655; PubMed=3303030;
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RA Lopez J.A., Chung D.W., Fujikawa K., Hagen F.S., Papayannopoulos T.,
 RA Roth G.U.;
 RT "Cloning of the alpha chain of human platelet glycoprotein Ib: a
 RT transmembrane protein with homology to leucine-rich alpha 2-
 RT glycoprotein."
 RL Proc. Natl. Acad. Sci. U.S.A. 84:5615-5619(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89025874; PubMed=2845978;
 RA Wenger R.H., Kieffer N., Wicks A.N., Clemetson K.J.;
 RT "Structure of the human blood platelet membrane glycoprotein Ib alpha
 RT gene."
 RL Biochem. Biophys. Res. Commun. 156:389-395(1988).
 RN [3]
 RP SEQUENCE FROM N.A., AND VARIANT PHE-86.
 RX MEDLINE=22034223; PubMed=12038791;
 RA Matsubara Y., Murata M., Moriki T., Yokoyama K., Matanabe N.,
 RA Nakajima H., Handa M., Kawano K., Aoki N., Yoshino H., Ikeda Y.;
 RT "A novel polymorphism, 70Leu/Phe, disrupts a consensus Leu residue
 RT within the leucine-rich repeat sequence of platelet glycoprotein
 RT Ibalph.";
 RL Thromb. Haemost. 87:867-872(2002).
 RN [4]
 RP SEQUENCE FROM N.A., AND VARIANT MET-161.
 RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
 RA Nickerson D.A.;
 RT "SeattleSNPs: NHLBI HUG6682 program for genomic applications, UW-
 RT FHCRC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";
 RN Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A., MUTAGENESIS OF GLY-249 AND MET-255, AND VARIANT
 RP PSEUDO-VWD SER-249.
 RX PubMed=14521605;
 RA Matsubara Y., Murata M., Sugita K., Ikeda Y.;
 RT "Identification of a novel point mutation in platelet glycoprotein
 RT Ibalph, Gly to Ser at residue 233, in a Japanese family with

RT platelet-type von Willebrand disease.";
RL J. Thromb. Haemost. 1:2198-2205(2003).
[6]
RN
RP SEQUENCE FROM N.A.
RC TISSUE=lung;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Tomihyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman B., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.M., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywicki M.I., Skalska U., Smalus D.E.,
RA Scherch A., Schein U.E., Jones S.U.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[7]
RN
RP SEQUENCE OF 17-315.
RX MEDLINE=87289654; PubMed=3497398;
RA Titani K., Takio K., Handa M., Ruggeri Z.M.,
RT "Amino acid sequence of the von Willebrand factor-binding domain of
platelet membrane glycoprotein Ib.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:5610-5614(1987).
[8]
RN
RP SEQUENCE OF 305-397 FROM N.A.
RX MEDLINE=97243178; PubMed=9086113;
RA Suzuki K., Hayashi T., Akiba J., Yahagi A., Tajima K., Satoh S.,
RA Sasaki H.,
RT "Styl polymorphism at nucleotide 1610 in the human platelet
glycoprotein Ib alpha gene.";
RL Jpn. J. Hum. Genet. 41:419-421(1996).
[9]
RN
RP DISULFIDE BONDS.
RX MEDLINE=91301149; PubMed=2070794;
RA Hess D., Schaller J., Rickli E.E., Clemenson K.U.,
RT "Identification of the disulphide bonds in human platelet
glycocalicin.";
RL Eur. J. Biochem. 199:389-393(1991).
[10]
RN
RP INTERACTION WITH FLNB.
RC TISSUE=Endothelial cells, and Placenta;
RX MEDLINE=9831317; PubMed=9651345; DOI=10.1074/jbc.273.28.17531;
RA Takakura T., Wu G., Murphy G.F., Shapiro S.S.,
RT "Human beta-1-taman is a new protein that interacts with the
cytoplasmic tail of glycoprotein Ibalphn.";
RL J. Biol. Chem. 273:17531-17538(1998).
[11]
RN
RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS).
RX MEDLINE=22171415; PubMed=12183630; DOI=10.1126/science.107355;
RA Holzinger E.G., Tsuji S., Komijn R.A., Schiphorst M.B., de Groot P.G.,
RA Sijma J.J., Gros P.,
RT "Structures of glycoprotein Ibalphn and its complex with von
Willebrand factor A1 domain.";
RL Science 297:1176-1179(2002).
[12]
RN
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 17-304, AND SULFATION OF
TYR-292; TYR-294 AND TYR-295.
RX MEDLINE=22217968; PubMed=12087105; DOI=10.1074/jbc.M205271200;
RA Uff S., Clemenson J.M., Harrison T., Clemenson K.J., Emley J.,
RT "Crystal structure of the platelet glycoprotein Ibalphn N-terminal
domain reveals an unmasking mechanism for receptor activation.";
RL J. Biol. Chem. 277:35657-35663(2002).
[13]

RP VARIANT SIBA MET-161.
RX MEDLINE=92265982; PubMed=1586750;
RA Murata M., Furuhata K., Ishida F., Russell S.R., Ware J.,
RA Ruggeri Z.M.,
RT "Genetic and structural characterization of an amino acid dimorphism
in glycoprotein Ib alpha involved in platelet transfection
refractoriness.";
RL Blood 79:3086-3090(1992).
[14]
RN
RP VARIANT BSS PHE-73.
RX MEDLINE=92110577; PubMed=1730088;
RA Miller U.L., Lyle V.A., Cunningham D.,
RT "Mutation of leucine-57 to phenylalanine in a platelet glycoprotein Ib
alpha leucine tandem repeat occurring in patients with an autosomal
dominant variant of Bernard-Soulier disease.";
RL Blood 79:439-446(1992).
[15]
RN
RP POLYMORPHISM OF PRO/THR-RICH DOMAIN.
RX MEDLINE=92250564; PubMed=1577776;
RA Lopez J.A., Ludwig E.H., McCarthy B.J.,
RT "Polymorphism of human glycoprotein Ib alpha results from a variable
number of tandem repeats of a 13-amino acid sequence in the mucin-like
macroglycopeptide region. Structure/function implications.";
RL J. Biol. Chem. 267:10055-10061(1992).
[16]
RN
RP VARIANT BSS VAL-172.
RX MEDLINE=93388851; PubMed=7690774;
RA Ware J., Russell S.R., Marchese P., Murata M., Mazzucato M.,
RA de Marco L., Ruggeri Z.M.,
RT "Point mutation in a leucine-rich repeat of platelet glycoprotein Ib
alpha resulting in the Bernard-Soulier syndrome.";
RL J. Clin. Invest. 92:1213-1220(1993).
[17]
RN
RP VARIANT BSS SER-225.
RX MEDLINE=95118882; PubMed=7819107;
RA Simek S., Norris P., Lozano M., Pico M., von Dem Borne A.E.G.K.,
RA Ribera A., Gallardo D.,
RT "Cy209 Ser mutation in the platelet membrane glycoprotein Ib alpha
gene is associated with Bernard-Soulier syndrome.";
RL Br. J. Haematol. 88:839-844(1994).
[18]
RN
RP VARIANT PSEUDO-VWD VAL-249.
RX MEDLINE=91271273; PubMed=2052556;
RA Miller J.L., Cunningham D., Lyle V.A., Finch C.N.,
RT "Mutation in the gene encoding the alpha chain of platelet
glycoprotein Ib in platelet-type von Willebrand disease.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:4761-4765(1991).
[19]
RN
RP VARIANT PSEUDO-VWD VAL-249.
RX MEDLINE=93253059; PubMed=8486780;
RA Murata M., Russell S.R., Ruggeri Z.M., Ware J.,
RT "Expression of the phenotypic abnormality of platelet-type von
Willebrand disease in a recombinant glycoprotein Ib alpha fragment.";
RL J. Clin. Invest. 91:2133-2137(1993).
[20]
RN
RP VARIANT PSEUDO-VWD VAL-255.
RX MEDLINE=93214031; PubMed=8384898;
RA Russell S.D., Roch G.J.,
RT "Pseudo-von Willebrand disease: a mutation in the platelet
glycoprotein Ib alpha gene associated with a hyperactive surface
receptor.";
RL Blood 81:1787-1791(1993).
[21]
RN
RP VARIANT SIBA MET-161, AND POLYMORPHISM OF PRO/THR-RICH DOMAIN.
RX PubMed=7632942;
RA Ishida F., Furuhata K., Ishida K., Yan J., Kitano K., Kiyosawa K.,
RA Furuta S.,
RT "The largest variant of platelet glycoprotein Ib alpha has four tandem
repeats of 13 amino acids in the macroglycopeptide region and a
genetic linkage with methionine145.";
RL Blood 86:1357-1360(1995).
[22]
RN
RP VARIANT BSS LEU-195 DEL.

```

RX MEDLINE=95178321; PubMed=7873390;
RA de la Salle C., Baas M.-J., Lanza F., Schwartz A., Hanau D.,
Query Match 100.0%; Score 44; DB 1; Length 626;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YDYPER 7
Db 292 YDYPER 298

RESULT 2
0742A0 PRELIMINARY; PRT; 945 AA.
AC 0742A0;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE AGR303WP.
GN ORFNames=AGR303W;
OS Ambya gossypii (Yeast) (Bremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Bremothecium.
OX NCBI_TaxID=33169;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 10895;
RA Lerch A., Brachat S., Voegel S.E., Gaffney T., Philippe P.,
RA Dietrich F.S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; A016820; AAS54793.1; -.
DR ACD; AGR303W; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004527; F:exonuclease activity; IEA.
DR InterPro; IPR004859; Puc_53exo.
DR Pfam; PF03159; XRN_N; 1.
SQ SEQUENCE 945 AA; 10768 MW; 6BFD78924E8FD166 CRC64;

Query Match 90.9%; Score 40; DB 2; Length 945;
Best Local Similarity 85.7%; Pred. No. 93;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YDYPER 7
Db 700 YDYPER 706

RESULT 3
OCUL_XENLA STANDARD; PRT; 493 AA.
ID OCUL_XENLA
AC 09PUN1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Occludin.
GN Name=OCUL;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A., AND PHOSPHORYLATION SITES THR-375 AND SER-379.
RC TISSUE=Ovary;
RX MEDLINE=99421641; PubMed=10491082;
RA Cordenonni M., Turco F., D'Acri F., Hammar E., Martinucci G.,
RA Meggio F., Citi S.;
RT "Xenopus laevis occludin. Identification of in vitro phosphorylation
sites by protein kinase CK2 and association with cingulin.";
RT Eur. J. Biochem. 264:374-384(1999).
RN [2]
RP CHARACTERIZATION.

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RX MEDLINE=98034414; PubMed=9365283;
RA Cordenonni M., Mazon E., De Rigo L., Baraldo S., Meggio F., Citi S.;
RT Occludin dephosphorylation in early development of Xenopus laevis.";
RL J. Cell Sci. 110:3131-3139(1997).
CC -1- FUNCTION: Probably plays a role in the formation and regulation of
CC the tight junction (rv) paracellular permeability barrier.
CC -1- SUBUNIT: Interacts in vitro with cingulin, possibly directly.
CC Interacts with ZO-1 (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Localized at tight junctions of both
CC epithelial and endothelial cells.
CC -1- DEVELOPMENTAL STAGE: A maternally synthesized protein. Found in
CC granules in the peripheral cytoplasm in the fertilized egg, it
CC localizes first to the basolateral membrane, then to tight
CC junctions after cingulin and ZO-1. Nascent tight junctions are in
CC place by the two-cell stage. The maternal form is more highly
CC phosphorylated than the form detected in later developmental
CC stages.
CC -1- DOMAIN: The C-terminus is cytoplasmic and is important for
CC interaction with ZO-1. Necessary for the tight junction
CC localization. Involved in the regulation of the permeability
CC barrier function of the tight junction (By similarity).
CC -1- PTM: Phosphorylated.
CC -1- SIMILARITY: Belongs to the EIL / occludin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC or send an email to license@isb.ch).
CC -----
DR EMBL; AF170275; AAD53725.1; -.
DR Inact; Q9PUN1; -.
DR InterPro; IPR008253; Marvel.
DR InterPro; IPR002958; Occludin.
DR InterPro; IPR010844; Occludin_EIL.
DR Pfam; PF01284; MARVEL; 1.
DR Pfam; PF07303; Occludin_EIL; 1.
DR PRINTS; PR01258; OCCLUDIN.
KM Coiled coil; Phosphorylation; Tight junction; Transmembrane.
FT DOMAIN 1 47
FT TRANSMEM 48 70
FT DOMAIN 71 116
FT TRANSMEM 117 141
FT DOMAIN 142 151
FT TRANSMEM 152 176
FT DOMAIN 177 224
FT TRANSMEM 225 246
FT DOMAIN 247 493
FT MOD RES 396 428
FT MOD RES 375 375
FT MOD RES 379 379
SQ SEQUENCE 493 AA; 5511 MW; 9694CD302BBBDE CRC64;

Query Match 86.4%; Score 38; DB 1; Length 493;
Best Local Similarity 85.7%; Pred. No. 11e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YDYPER 7
Db 25 YDYPER 31

RESULT 4
09KMJ7 PRELIMINARY; PRT; 161 AA.
AC 09KMJ7;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein yvgK (fragment).

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GN Name=yv9X;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MJ3;
RX MEDLINE=2015229; PubMed=10708580; DOI=10.1006/bbrc.2000.2277;
RA Kuroda M., Kuzhara-Arai K., Hiramatsu K.;
RT "Identification of the up- and down-regulated genes in vancomycin-resistant Staphylococcus aureus strains MJ3 and MJ50 by cDNA differential hybridization method.";
RT Biochem. Biophys. Res. Commun. 269:485-490(2000).
RL EMBL; AB035451; BAB0335.1; -;
DR HSSP; O32220; 1K0K.
DR GO; GO:0015097; F:mercury ion transporter activity; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0015694; P:mercury ion transport; IEA.
DR GO; GO:0030001; P:metal ion transport; IEA.
DR InterPro; IPR006121; HeavyMe.transpt.
DR InterPro; IPR001802; HG.scavenger.
DR InterPro; IPR006191; Metal_bind.
DR Pfam; PF00403; HMA; 2.
DR PRINTS; PR00946; HGSCAVENGER.
DR PROSITE; PS01047; HMA_1; 2.
DR PROSITE; PS0846; HMA_2; 2.
KM Hypothetical protein.
FT NON_TER 161
SQ SEQUENCE 161 AA; 17939 MW; 339B440D24C36C CRC64;

Query Match 84.1%; Score 37; DB 2; Length 161;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYPPER 7
Db 115 DYPPER 120

RESULT 5
Q86TNO PRELIMINARY; PRT; 232 AA.
ID Q86TNO
AC Q86TNO; (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Similar to Kruppel-like factor 3 (basic).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner F.S., Shemen C.M., Schler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko U., Marusik A., Farmer A.F., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Tohilyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywnicki M.I., Skalska U., Smalins D.E., Schmech A., Schein J.E.,
RA Jones S.J., Matra M.A.;
"Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX Strausberg R.;
RL Submitted (Apr-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC051687; AAH51687.1; -;
SQ SEQUENCE 232 AA; 25529 MW; 70AA00DA831A5D6B CRC64;

Query Match 84.1%; Score 37; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYPPER 7
Db 209 DYPPER 214

RESULT 6
Q8BV07 PRELIMINARY; PRT; 274 AA.
ID Q8BV07
AC Q8BV07; (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone:Cl30019K13 product:Kruppel-like factor 3 (basic), full insert sequence. (Fragment).
DE Name=Klf3;
GN Name=Klf3;
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN PANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RA The PANTOM Consortium;
RT "The RIKEN Genome Exploration Research Group Phase I & II Team; Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=20330913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Atawa K., Nagaoka S., Sasaki N., Carninci P., Kono H., Akiyama Y., Nishi K., Kitsuai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara B., Watabiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.,
 RT "RIKEN Integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.",
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirozane T.,
 RA Hori F., Imocant K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK081467; BAC3827.1; -.
 DR HSSP; Q60980; 1P7A.
 DR MGD; MGI:1342773; Klf3.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003676; P:nucleic acid binding; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00096; zf-C2H2; 3.
 DR ProDom; PD000003; Znf_C2H2; 3.
 DR SMART; SM00355; Znf_C2H2; 3.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
 DR PROSITE; PSS015; ZINC_FINGER_C2H2_2; 3.
 RT NON-TER 1
 SQ SEQUENCE 274 AA; 30721 MW; 86FA8C7AD7D8E707 CRC64;
 QY
 Db 138 DYPPEE 143
 2 DYPPEE 7
 |||||
 Query Match 84.1%; Score 37; DB 2; Length 274;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
 Q8PXU9 PRELIMINARY; PRT; 301 AA.
 AC Q8PXU9;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Polysaccharide deacetylase (EC 3.5.1.-).
 GN OrderedLocNames=WM1117;
 OS Methanosarcina mazei (Methanosarcina frisia).
 OC Archaea; Euryarchaeota; Methanocicrobia; Methanosarcinales;
 OC Methanosarcinaceae; Methanosarcina.
 NCBI_TaxID=2209;
 OX [1]
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=Goe1 / ATCC BAA-199 / DSM 3647 / OCM 88;
 RA MEDLINE=22120827; PubMed=12125824;
 RX Depkenmeier U., Johann A., Hartesch T., Merk R., Schmitz R.A.,
 RA Martinez-Arias R., Henne A., Wierzer A., Bauner S., Jacobl C.,
 RA Brueggemann H., Ilenard T., Christmann A., Boemecke M., Steckel S.,
 RA Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
 RA Filtz H.-J., Gottschalk G.;
 RT "The genome of Methanosarcina mazei: evidence for lateral gene
 RT transfer between Bacteria and Archaea.";
 RL J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
 DR EMBL; AE013339; AAM30813.1; -.
 DR GO; GO:001610; P:hydrolase activity, acting on carbon-nitrog. . .; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.

DR InterPro; IPR002509; Polysac deacc.
 DR Pfam; PF01522; Polysacc_deac_1; 1.
 KW Complete proteome.
 SQ SEQUENCE 301 AA; 34521 MW; 4D1DA3869C9BCCB CRC64;
 QY
 Db 181 YDYPPEE 187
 1 YDYPPEE 7
 |||||
 Query Match 84.1%; Score 37; DB 2; Length 301;
 Best Local Similarity 85.7%; Pred. No. 1e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 8
 Q9HHP9 PRELIMINARY; PRT; 305 AA.
 AC Q9HHP9;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Vng6290h.
 GN OrderedLocNames=VNG6290H;
 OS Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
 OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
 OC Halobacteriaceae; Halobacterium.
 OX NCBI_TaxID=64091;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20504483; PubMed=11016950; DOI=10.1073/pnas.190337797;
 RA Ng W.V., Kennedy S.P., Nhaliras G.G., Bergius B., Pan M.,
 RA Shukla H.D., Lasky S.R., Balliga N.S., Thorsson V., Sirogna J.,
 RA Swartzell S., Weir D., Hall J., Dahl T.A., Weltl R., Goo Y.A.,
 RA Leitbauer B., Keller K., Cruz R., Danson M.J., Hough D.W.,
 RA Maddocks D.G., Jablonki P.E., Krebs M.P., Angvine C.M., Dale K.,
 RA Isebnarger T.A., Peck R.F., Pohlischer M., Spudich J.L., Jung K.-H.,
 RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
 RA Ebdardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
 RT "Genome sequence of Halobacterium species NRC-1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
 DR EMBL; AE005159; AAG20927.1; -.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0004603; F:transposase activity; IEA.
 DR GO; GO:0006313; P:DNA transposition; IEA.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR002559; Transposase_11.
 DR Pfam; PF01609; Transposase_11; 1.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
 KW Complete proteome; Plasmid.
 SQ SEQUENCE 305 AA; 35424 MW; 65D41B43E6EDF3B3 CRC64;
 QY
 Db 18 YDYPPEE 7
 |||||
 Query Match 84.1%; Score 37; DB 2; Length 305;
 Best Local Similarity 71.4%; Pred. No. 1e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 9
 KLF3 MOUSE STANDARD; PRT; 344 AA.
 ID KLF3 MOUSE
 AC Q60960;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Kruppel-like factor 3 (Basic Kruppel-like factor) (CAACC-box binding
 DE protein KLF) (TFF-2).
 GN Name=KLF3; Synonyms=BKLF;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RX [1]
RP SEQUENCE FROM N.A.; FUNCTION, AND TISSUE SPECIFICITY.
RC STRAIN=DNA; TISSUE=Leukemia;
RX MEDLINE=9629326; PubMed=8657145;
RA Crossley M., Whitelaw B., Perkins A., Williams G., Fujiwara Y.,
Orkin S.H.;
RT "Isolation and characterization of the cDNA encoding BKL/TF-2, a
major CACCC-box-binding protein in erythroid cells and selected other
cells."
RL Mol. Cell. Biol. 16:1695-1705(1996).
CC -1- FUNCTION: Binds to the CACCC box. May play a role in
hematopoiesis.
CC -1- SUBUNIT: Interacts with the C-terminal binding protein 2.
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- TISSUE SPECIFICITY: In 8.5 day embryos, expressed in midbrain,
anterior hindbrain and ventral anterior half of embryo including
expressed throughout ventral anterior half of embryo including
midbrain-hindbrain junction, ventral midbrain, diencephalon and
forebrain. At 10.5 days, distribution is more widespread with
expression also found in developing limb buds. Widely expressed in
the adult.
CC -1- SIMILARITY: Belongs to the kruppel C2H2-type zinc-finger protein
family.
CC -1- SIMILARITY: Contains 3 C2H2-type zinc fingers.
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or send an email to license@isb-sib.ch).

DR EMBL: U96340; AAA93256.1; --
DR PIR: J06100; J06100.
DR PDB: 1P7A; NMR; A=308-344.
DR MGD: MGI:134273; Klf3.
DR InterPro: IPR007087; Znf.C2H2.
DR Pfam: PF00096; zf-C2H2; 3.
DR ProDom: PD000003; Znf.C2H2; 3.
DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 3.
DR PROSITE: PS50157; ZINC_FINGER_C2H2_2; 3.
KW 3D-structure; Activator; DNA-binding; Metal-binding; Nuclear protein;
KM Repeat; Repressor; Transcription regulation; Zinc-finger.
FT DOMAIN 1 250 Pro-rich.
FT SITE 1 74 Repressor domain.
FT SITE 61 65 CTBP-binding motif.
FT ZN_FING 259 283 C2H2-type 1.
FT ZN_FING 289 313 C2H2-type 2.
FT ZN_FING 319 341 C2H2-type 3.
SQ SEQUENCE 344 AA; 38560 MW; 2B7E3B63A7C1D88 CRC64;

Query Match 84.1%; Score 37; DB 1; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYPPEE 7
DB 208 DYPPEE 213

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
ON NCBI_TaxID=9606;
RX [1]
RP SEQUENCE FROM N.A.
RA Matsumoto N., Yoshida T., Terada M.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RC SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Qu X., Zhang C., Wang M., Yu Y., Wei H., Xing G., Wu S., Zhai Y.,
Lu C., Zhou G., Dong C., He F.;
RT "BKL/TF mRNA for basic Kruppel-like factor."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Binds to the CACCC box. May play a role in hematopoiesis
(By similarity).
CC -1- SUBUNIT: Interacts with the C-terminal binding protein 2 (By
similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- SIMILARITY: Belongs to the kruppel C2H2-type zinc-finger protein
family.
CC -1- SIMILARITY: Contains 3 C2H2-type zinc fingers.
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DR EMBL: AB024523; BAA92271.1; --
DR EMBL: AF285837; AAK27329.1; --
DR HSRF: P08047; ISP2.
DR Genew: HGNC:16516; KLF3.
DR GO: GO:0007275; P:development; TAS.
DR InterPro: IPR007087; Znf.C2H2.
DR Pfam: PF00096; zf-C2H2; 3.
DR ProDom: PD000003; Znf.C2H2; 3.
DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 3.
DR PROSITE: PS50157; ZINC_FINGER_C2H2_2; 3.
KW Activator; DNA-binding; Metal-binding; Nuclear protein; Repeat;
KM Repressor; Transcription regulation; Zinc-finger.
FT DOMAIN 1 251 Pro-rich.
FT SITE 1 74 Repressor domain.
FT SITE 61 65 CTBP-binding motif.
FT ZN_FING 260 284 C2H2-type 1.
FT ZN_FING 290 314 C2H2-type 2.
FT ZN_FING 320 342 C2H2-type 3.
SQ SEQUENCE 345 AA; 38828 MW; A490D642AB8F1FDC CRC64;

Query Match 84.1%; Score 37; DB 1; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYPPEE 7
DB 209 DYPPEE 214

RESULT 11
ID OGPRI PRELIMINARY; PRT; 345 AA.
AC OGPRI;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Kruppel-like factor 3 (Basic).
GN Name=KLF3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

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DR EMBL; AE017261; AAT42643.1; -
SQ COMPLETE proteome; Hypothetical protein.
SQ SEQUENCE 431 AA; 50746 MW; F24F79E7E7F0C40F CRC64;

Query Match
Best Local Similarity 84.1%; Score 37; DB 2; Length 431;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYPYEE 7
   |||||
Db 101 YDFYPOE 107

RESULT 13
O962Y5 PRELIMINARY; PRT; 441 AA.
ID O962Y5
AC O962Y5
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Putative chitinase (EC 3.2.1.14) (Fragment).
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridoidea;
OC Ascarididae; Ascaris.
CC NCBI_TaxID=6253;
CX [1]
RN
RP SEQUENCE FROM N.A.
RA Geng J., Komuniecki P., Komuniecki R.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF395836; AAK3964.1; -.
DR HSSP; P23951; ICNS.
DR GO; GO:0004568; F:chitinase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0016988; P:cell wall catabolism; IEA.
DR GO; GO:0006032; P:chitin catabolism; IEA.
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00182; Glyco_hydro_19; 1.
KW Glycosidase; Hydrolase.
FT NCV TER
SQ SEQUENCE 441 AA; 49416 MW; C1EF9BE91D2B65B1 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DYPYEE 7
   |||||
Db 392 DYPYEE 397

RESULT 14
O8AA14 PRELIMINARY; PRT; 468 AA.
ID O8AA14
AC O8AA14
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Glycosyltransferase.
OS OrderedLocustNames=BY0480;
OC Bacteroides thetaiotaomicron.
OC Bacteriia; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
CC NCBI_TaxID=818;
CX [1]
RN
RP SEQUENCE FROM N.A.
RA STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=32550858; PubMed=12663928; DOI=10.1126/science.1080029;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
Chiang H.C., Hooper J.V., Gordon J.I.,
"A genomic view of the human-Bacteroides thetaiotaomicron symbiosis."
Science 299:2074-2076(2003).

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DR EMBL; AE016927; AAC75587.1; -.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR InterPro; IPR003362; Bact_transf.
 DR Pfam; PF02397; Bact_transf_1.
 KM Complete proteome; Transferase.
 SQ SEQUENCE 468 AA; 55016 MW; 7DAA3596275C8907 CRC64;

Query Match 84.1%; Score 37; DB 2; Length 468;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYPPEE 7
 |||||
 Db 181 DYPPEE 186

RESULT 15

O9KR88 PRELIMINARY; PRT; 547 AA.
 ID O9KR88
 AC O9KR88;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Paragut-inducible protein B.
 GN OrderedLocustNames=VCI1754;
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrrio.
 OX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=El Tor N16961 / Serotype O1;
 RX MEDLINE=20406833; PubMed=10952301; DOI=10.1038/35020000;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
 Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.L.,
 Ermolaeva M.D., Vamathevan J.J., Bass S., Qin H., Dragoi I.,
 Selens P., McDonald L.A., Utterback T.R., Fleischmann R.D.,
 Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R.,
 Mekalanos J.J., Venter J.C., Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 cholerae";
 RL Nature 406:477-483(2000).
 DR EMBL; AE004252; AAF94904.1; -.
 DR PIR; F82162; F82162.
 DR TIGR; VCI1754; -.
 KM Complete proteome.
 SQ SEQUENCE 547 AA; 60897 MW; 32FC58F0B6A4B72D CRC64;

Query Match 84.1%; Score 37; DB 2; Length 547;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYPPEE 7
 |||||
 Db 395 DYPPEE 400

Search completed: September 9, 2005, 16:30:40
 Job time : 102.1 secs

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OM protein - protein search, using SW model

Run on: September 9, 2005, 15:47:04 ; Search time 28 Seconds

(Without alignments)
18.662 Million cell updates/sec

Title: US-10-032-037C-266

Perfect score: 44

Sequence: 1 YDYPERE 7

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents AA:*

1: /cgn2_6/prodata/1/aa/5A_COMB.pep.*
2: /cgn2_6/prodata/1/aa/5B_COMB.pep.*
3: /cgn2_6/prodata/1/aa/5A_COMB.pep.*
4: /cgn2_6/prodata/1/aa/5B_COMB.pep.*
5: /cgn2_6/prodata/1/aa/PCUS_COMB.pep.*
6: /cgn2_6/prodata/1/aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	19	1	US-08-520-977A-8
2	44	100.0	60	4	US-09-381-546-15
3	44	100.0	61	4	US-09-381-546-11
4	44	100.0	63	4	US-09-381-546-16
5	44	100.0	66	4	US-09-381-546-45
6	44	100.0	320	1	US-07-813-083B-1
7	44	100.0	610	1	US-07-821-717B-6
8	44	100.0	610	1	US-08-119-262B-6
9	44	100.0	610	1	US-08-135-829A-11
10	44	100.0	610	1	US-08-234-265A-11
11	37	84.1	344	1	US-08-843-993-3
12	37	84.1	344	3	US-09-059-520A-3
13	37	84.1	344	3	US-09-334-275-3
14	37	84.1	345	3	US-08-843-993-1
15	37	84.1	345	3	US-09-059-520A-1
16	37	84.1	345	3	US-09-334-275-1
17	37	84.1	749	4	US-09-562-737-91
18	37	84.1	749	4	US-09-562-737-92
19	37	84.1	749	4	US-09-562-737-93
20	37	84.1	749	4	US-09-562-737-94
21	36	81.8	1327	4	US-09-270-767-57925
22	36	81.8	316	4	US-09-270-767-42611
23	35	79.5	3421	4	US-09-452-638-53
24	34	77.3	75	4	US-09-107-532A-6815
25	34	77.3	131	4	US-09-270-767-61319
26	34	77.3	166	4	US-09-270-767-45796
27	34	77.3	173	6	5196333-6

28	34	77.3	173	6	5196333-6	Patent No. 5196333
29	34	77.3	294	6	5196333-2	Patent No. 5196333
30	34	77.3	294	6	5196333-2	Patent No. 5196333
31	34	77.3	339	4	US-09-902-540-13163	Sequence 13163, A
32	34	77.3	539	4	US-09-248-796A-20047	Sequence 20047, A
33	34	77.3	627	4	US-09-489-039A-12782	Sequence 12782, A
34	34	77.3	667	4	US-09-248-796A-22880	Sequence 22880, A
35	34	77.3	749	4	US-09-562-737-99	Sequence 99, Appl
36	33	75.0	210	4	US-09-903-456-68	Sequence 68, Appl
37	33	75.0	243	4	US-09-508-710-18	Sequence 18, Appl
38	33	75.0	459	4	US-09-270-767-45596	Sequence 45596, A
39	33	75.0	757	4	US-09-107-532A-7189	Sequence 7189, Ap
40	33	75.0	873	3	US-08-990-140-2	Sequence 2, Appl
41	33	75.0	873	3	US-09-546-238-2	Sequence 3607, Ap
42	32	72.7	168	4	US-09-134-000C-3607	Sequence 1678, Ap
43	32	72.7	247	4	US-09-710-279-1678	Sequence 3, Appl
44	32	72.7	291	4	US-09-495-406-3	Sequence 5, Appl
45	32	72.7	291	4	US-09-495-406-5	

ALIGNMENTS

RESULT 1
US-08-520-977A-8
Sequence 8, Application US/08520977A
Patent No. 5659018
GENERAL INFORMATION:
APPLICANT: Berndt, Michael C.
APPLICANT: Dunlop, Lindsay
APPLICANT: Andrews, Robert
APPLICANT: Deluca, Mariagrazia
TITLE OF INVENTION: MOCARHAGIN, A NOVEL COBRA VENOM
TITLE OF INVENTION: PROTEASE, AND THERAPEUTIC USES THEREOF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSER: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,977A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-520-977A-8
Query Match 100.0%; Score 44; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 YDYPERE 7
|||||||

Db 8 YDYPER 14

RESULT 2

US-09-381-546-15
; Sequence 15, Application US/09381546
; Patent No. 6451976
; GENERAL INFORMATION:
; APPLICANT: Trigen Limited
; TITLE OF INVENTION: BI- OR MULTIFUNCTIONAL MOLECULES BASED ON A DENDROASPIN
; FILE REFERENCE: P41007MO
; CURRENT FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: PCT/GB98/00848
; PRIOR FILING DATE: 1998-09-20
; PRIOR APPLICATION NUMBER: GB9705787.1
; PRIOR FILING DATE: 1997-03-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: modified
US-09-381-546-15

Query Match 100.0%; Score 44; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 0.87;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YDYPER 7
|||||
Db 28 YDYPER 34

RESULT 3

US-09-381-546-11
; Sequence 11, Application US/09381546
; Patent No. 6451976
; GENERAL INFORMATION:
; APPLICANT: Trigen Limited
; TITLE OF INVENTION: BI- OR MULTIFUNCTIONAL MOLECULES BASED ON A DENDROASPIN
; FILE REFERENCE: P41007MO
; CURRENT FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: PCT/GB98/00848
; PRIOR FILING DATE: 1998-09-20
; PRIOR APPLICATION NUMBER: GB9705787.1
; PRIOR FILING DATE: 1997-03-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: modified
US-09-381-546-11

Query Match 100.0%; Score 44; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YDYPER 7
|||||
Db 9 YDYPER 15

RESULT 4

US-09-381-546-16
; Sequence 16, Application US/09381546
; Patent No. 6451976
; GENERAL INFORMATION:
; APPLICANT: Trigen Limited
; TITLE OF INVENTION: BI- OR MULTIFUNCTIONAL MOLECULES BASED ON A DENDROASPIN
; FILE REFERENCE: P41007MO
; CURRENT FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: PCT/GB98/00848
; PRIOR FILING DATE: 1998-09-20
; PRIOR APPLICATION NUMBER: GB9705787.1
; PRIOR FILING DATE: 1997-03-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: modified
US-09-381-546-16

Query Match 100.0%; Score 44; DB 4; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.92;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YDYPER 7
|||||
Db 28 YDYPER 34

RESULT 5

US-09-381-546-45
; Sequence 45, Application US/09381546
; Patent No. 6451976
; GENERAL INFORMATION:
; APPLICANT: Trigen Limited
; TITLE OF INVENTION: BI- OR MULTIFUNCTIONAL MOLECULES BASED ON A DENDROASPIN
; FILE REFERENCE: P41007MO
; CURRENT FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: PCT/GB98/00848
; PRIOR FILING DATE: 1998-09-20
; PRIOR APPLICATION NUMBER: GB9705787.1
; PRIOR FILING DATE: 1997-03-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: modified
US-09-381-546-45

Query Match 100.0%; Score 44; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YDYPER 7
|||||
Db 57 YDYPER 63

RESULT 6

US-07-613-083B-1
; Sequence 1, Application US/07613083B

```

; Patent No. 5340727
; GENERAL INFORMATION:
; APPLICANT: Ruggeri, Zaverio M.
; APPLICANT: Ware, Jerry, Inventors
; APPLICANT: on behalf of Scripps Clinic and Research
; APPLICANT: Foundation
; TITLE OF INVENTION: GP1b' Fragments and Recombinant
; TITLE OF INVENTION: DNA Expression Vectors
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scripps Clinic and Research
; ADDRESSEE: Foundation
; STREET: 10666 No. 5340727ch Torrey Pines Road
; CITY: La Jolla
; STATE: California
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette-5.25 inch, 1.2 Mb
; COMPUTER: AST Bravo IBM PC comp. (386SX)
; OPERATING SYSTEM: MS DOS version 3.2
; SOFTWARE: Wordperfect 5.1 conv. to ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/613,083B
; FILING DATE: 19911114
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: This appl. is a c-i-p of
; APPLICATION NUMBER: U.S. 07/470,674
; FILING DATE: 04-Jan-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Barron, Alexis
; REGISTRATION NUMBER: 22,702
; REFERENCE/DOCKET NUMBER: P16,569-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 923-4466
; TELEFAX: (215) 923-2189
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 320
; TYPE: AMINO ACID
; STRANDEDNESS: No. 5340727 applicable
; TOPOLOGY: Linear
; US-07-613-083B-1
;
Query Match 100.0%; Score 44; DB 1; Length 320;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 YDYYPEE 7
Db 276 YDYYPEE 282
;
RESULT 7
US-07-821-717B-6
; Sequence 6, Application US/07821717B
; Patent No. 5296239
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Cunningham, David
; APPLICANT: Lyle, Vicki A.
; APPLICANT: Finch, Clara N.
; TITLE OF INVENTION: MUTATIONS RENDERING PLATELET
; TITLE OF INVENTION: GLYCOPROTEIN Ib ALPHA LESS REACTIVE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/821,717B
; FILING DATE: 15-JAN-1992
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Timain, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 610 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PUBLICATION INFORMATION:
; AUTHORS: Lopez, Jose A.
; AUTHORS: Chung, Dominic W.
; AUTHORS: Fujikawa, Kazuo
; AUTHORS: Hagen, Frederick S.
; AUTHORS: Papayannopoulou, Thalia
; AUTHORS: Roth, Gerald J.
; TITLE: Cloning of the alpha chain of human
; TITLE: platelet glycoprotein Ib: A transmembrane protein with homology
; TITLE: to leucine-rich alpha-2-glycoprotein
; JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
; VOLUME: 84
; PAGES: 5615-5619
; DATE: AUG-1987
; RELEVANT RESIDUES IN SEQ ID NO: 6: FROM 0 TO 610
; PUBLICATION INFORMATION:
; AUTHORS: Zimmerman, Theodore S.
; AUTHORS: Ruggeri, Zaverio M.
; AUTHORS: Houghten, Richard A.
; AUTHORS: Vincete, Vincete
; AUTHORS: Mohri, Hiroshi
; TITLE: Proteolytic fragments and synthetic
; TITLE: peptides that block the binding of von Willebrand factor to the
; TITLE: platelet membrane glycoprotein Ib
; DOCUMENT NUMBER: EP 0 317 278 A2
; FILING DATE: 16-NOV-1988
; PUBLICATION DATE: 24-MAY-1989
; RELEVANT RESIDUES IN SEQ ID NO: 6: FROM 0 TO 293
; US-07-821-717B-6
;
Query Match 100.0%; Score 44; DB 1; Length 610;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 YDYYPEE 7
Db 276 YDYYPEE 282
;
RESULT 8
US-08-119-262B-6
; Sequence 6, Application US/08119262B
; Patent No. 5492809
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Cunningham, David
; APPLICANT: Lyle, Vicki A.
; APPLICANT: Finch, Clara N.
; TITLE OF INVENTION: MUTATIONS RENDERING PLATELET
; TITLE OF INVENTION: GLYCOPROTEIN Ib ALPHA LESS REACTIVE
; NUMBER OF SEQUENCES: 6

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;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
;; STREET: Clinton Square, P.O. Box 1051
;; CITY: Rochester
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 14603
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: IBM PC compatible
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/119,262B
;; FILING DATE: 09-SEP-1993
;; CLASSIFICATION: 424
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US 07/821,717
;; FILING DATE: 15-JAN-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Timian, Susan J.
;; REGISTRATION NUMBER: 34,103
;; REFERENCE/DOCKET NUMBER: 20884/22
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (716) 263-1636
;; TELEFAX: (716) 263-1600
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 610 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; PUBLICATION INFORMATION:
;; AUTHORS: Lopez, Jose A.
;; AUTHORS: Chung, Dominic W.
;; AUTHORS: Fujikawa, Kazuo
;; AUTHORS: Hagen, Frederick S.
;; AUTHORS: Papayannopoulou, Thalia
;; AUTHORS: Roth, Gerald J.
;; TITLE: Cloning of the alpha chain of human platelet
;; TITLE: glycoprotein Ib: A transmembrane protein
;; TITLE: leucine-rich alpha-2-glycoprotein
;; JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
;; VOLUME: 84
;; PAGES: 5615-5619
;; DATE: AUG-1987
;; RELEVANT RESIDUES IN SEQ ID NO: 6: FROM 0 TO 610
;; PUBLICATION INFORMATION:
;; AUTHORS: Zimmerman, Theodore S.
;; AUTHORS: Ruggeri, Zaverio M.
;; AUTHORS: Houghten, Richard A.
;; AUTHORS: Vincete, Vincete
;; AUTHORS: Mohri, Hiroshi
;; TITLE: Proteolytic fragments and synthetic peptides
;; TITLE: that block the binding of von Willebrand
;; TITLE: membrane glycoprotein Ib
;; DOCUMENT NUMBER: EP 0 317 278 A2
;; FILING DATE: 16-NOV-1988
;; PUBLICATION DATE: 24-MAY-1989
;; RELEVANT RESIDUES IN SEQ ID NO: 6: FROM 0 TO 293
;; US-08-119-262B-6

Query Match 100.0%; Score 44; DB 1; Length 610;
Best Local Similarity 100.0%; Pred. No. 9.2; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YDYYPEE 7
Db 276 YDYYPEE 282

RESULT 9

;; US-08-135-929A-11
;; Sequence 11, Application US/08135929A
;; Patent No. 5593959
;; GENERAL INFORMATION:
;; APPLICANT: Miller, Jonathan L.
;; APPLICANT: Cunningham, David
;; APPLICANT: Lyle, Vicki A.
;; APPLICANT: Finch, Clara N.
;; APPLICANT: Pincus, Matthew R.
;; TITLE OF INVENTION: Mutations in the Gene Encoding the Alpha
;; TITLE OF INVENTION: Chain of Platelet Glycoprotein Ib
;; NUMBER OF SEQUENCES: 11
;; CORRESPONDENCE ADDRESSES:
;; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
;; STREET: Clinton Square, P.O. Box 1051
;; CITY: Rochester
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 14603
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: IBM PC compatible
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/135,929A
;; FILING DATE: 14-OCT-1993
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Timian, Susan J.
;; REGISTRATION NUMBER: 34,103
;; REFERENCE/DOCKET NUMBER: 20884/23
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (716) 263-1636
;; TELEFAX: (716) 263-1600
;; TELEX: 978450
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 610 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-135-929A-11

Query Match 100.0%; Score 44; DB 1; Length 610;
Best Local Similarity 100.0%; Pred. No. 9.2; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YDYYPEE 7
Db 276 YDYYPEE 282

RESULT 10
US-08-234-265A-11
Sequence 11, Application US/08234265A
Patent No. 5624817
GENERAL INFORMATION:
APPLICANT: Miller, Jonathan L.
APPLICANT: Cunningham, David
APPLICANT: Lyle, Vicki A.
APPLICANT: Finch, Clara N.
APPLICANT: Pincus, Matthew R.
TITLE OF INVENTION: Mutations in the Gene Encoding the
TITLE OF INVENTION: Chain of Platelet Glycoprotein Ib
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/234,265A
FILING DATE: 28-APR-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Timlan, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 20884/24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
TELEX: 978450
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 610 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-234-265A-11

Query Match 100.0%; Score 44; DB 1; Length 610;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYDYPPEE 7
Db 276 YDYDPEE 282

RESULT 11
US-08-843-993-3
Sequence 3, Application US/08843993
Patent No. 5739010
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: HUMAN TRANSCRIPTION FACTOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,993
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0274 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 344 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1244515
US-08-843-993-3

Query Match 84.1%; Score 37; DB 1; Length 344;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DYDYPPEE 7
Db 208 DYDYPPEE 213

RESULT 12
US-09-059-520A-3
Sequence 3, Application US/09059520A
Patent No. 6001971
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: HUMAN TRANSCRIPTION FACTOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/059,520A
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0274 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 344 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1244515
US-09-059-520A-3

Query Match 84.1%; Score 37; DB 3; Length 344;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DYDYPPEE 7
Db 208 DYDYPPEE 213

RESULT 13
US-09-334-275-3
Sequence 3, Application US/09334275
Patent No. 6037132

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; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: HUMAN TRANSCRIPTION FACTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: IBM Compatible
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/334,275
; FILING DATE:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 09/059,520
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0274 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1244515
;
US-09-334-275-3

Query Match      84.1%; Score 37; DB 3; Length 344;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DYPPEE 7
DB      208 DYPPEE 213

RESULT 14
US-08-843-993-1
; Sequence 1, Application US/08843993
; Patent No. 5739010
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: HUMAN TRANSCRIPTION FACTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: IBM Compatible
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/843,993

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; FILING DATE: Filed Herewith
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0274 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 345 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SYN00AT01
; CLONE: 727885
;
US-08-843-993-1

Query Match      84.1%; Score 37; DB 1; Length 345;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DYPPEE 7
DB      209 DYPPEE 214

RESULT 15
US-09-059-520A-1
; Sequence 1, Application US/09059520A
; Patent No. 6001971
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: HUMAN TRANSCRIPTION FACTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: IBM Compatible
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/059,520A
; FILING DATE: Filed Herewith
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0274 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 345 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SYN00AT01

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CLONE: 727885
US-09-059-520A-1

Query Match 84.1%; Score 37; DB 3; Length 345;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DYPPEE 7
Db 209 DYPPEE 214

Search completed: September 9, 2005, 15:57:56
Job time : 29 secs

Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 9, 2005, 15:52:48 ; Search time 106.75 Seconds

(without alignments)
25.864 Million cell updates/sec

Title: US-10-032-037C-266

Perfect score: 44

Sequence: 1 YDYYPE 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1777461 seqs, 394431504 residues

Total number of hits satisfying chosen parameters: 1777461

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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22: /cgn2_6/prodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	100.0	18	17	US-10-880-922-43
2	44	100.0	18	17	US-10-880-922-44
3	44	100.0	18	17	US-10-880-922-50
4	44	100.0	18	17	US-10-880-922-57
5	44	100.0	18	17	US-10-880-922-58
6	44	100.0	19	18	US-10-880-922-55
7	44	100.0	19	18	US-10-881-405-22
8	44	100.0	66	9	US-09-779-054-14
9	44	100.0	66	15	US-10-467-020-15
10	44	100.0	290	14	US-10-068-426-10
11	44	100.0	290	14	US-10-068-426-11
			290	14	US-10-068-426-12

12	44	100.0	290	15	US-10-382-758-10	Sequence 10, Appl
13	44	100.0	290	15	US-10-382-758-11	Sequence 11, Appl
14	44	100.0	290	15	US-10-382-758-12	Sequence 12, Appl
15	44	100.0	290	17	US-10-868-371-1	Sequence 1, Appl
16	44	100.0	290	17	US-10-868-371-2	Sequence 2, Appl
17	44	100.0	290	17	US-10-868-371-6	Sequence 6, Appl
18	44	100.0	301	14	US-10-068-426-9	Sequence 9, Appl
19	44	100.0	301	15	US-10-382-758-9	Sequence 9, Appl
20	44	100.0	301	17	US-10-868-371-5	Sequence 5, Appl
21	44	100.0	302	14	US-10-068-426-7	Sequence 7, Appl
22	44	100.0	302	14	US-10-068-426-8	Sequence 8, Appl
23	44	100.0	302	15	US-10-382-758-7	Sequence 7, Appl
24	44	100.0	302	15	US-10-382-758-8	Sequence 8, Appl
25	44	100.0	302	17	US-10-868-371-3	Sequence 3, Appl
26	44	100.0	302	17	US-10-868-371-4	Sequence 4, Appl
27	44	100.0	307	17	US-10-868-371-7	Sequence 7, Appl
28	44	100.0	531	14	US-10-068-426-4	Sequence 4, Appl
29	44	100.0	531	14	US-10-068-426-5	Sequence 5, Appl
30	44	100.0	531	14	US-10-068-426-6	Sequence 6, Appl
31	44	100.0	531	15	US-10-382-758-4	Sequence 4, Appl
32	44	100.0	531	15	US-10-382-758-5	Sequence 5, Appl
33	44	100.0	531	15	US-10-382-758-6	Sequence 6, Appl
34	44	100.0	544	14	US-10-068-426-1	Sequence 1, Appl
35	44	100.0	544	14	US-10-068-426-2	Sequence 2, Appl
36	44	100.0	544	14	US-10-068-426-3	Sequence 3, Appl
37	44	100.0	544	15	US-10-382-758-1	Sequence 1, Appl
38	44	100.0	544	15	US-10-382-758-2	Sequence 2, Appl
39	44	100.0	544	15	US-10-382-758-3	Sequence 3, Appl
40	44	100.0	562	16	US-10-825-127-7	Sequence 7, Appl
41	44	100.0	568	16	US-10-825-127-14	Sequence 14, Appl
42	44	100.0	610	20	US-11-053-199-2	Sequence 2, Appl
43	44	100.0	626	16	US-10-408-765A-430	Sequence 430, App
44	44	100.0	626	17	US-10-741-600-1496	Sequence 1496, Ap
45	39	88.6	8	18	US-10-881-405-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-10-880-922-43

Sequence 43, Application US/10880922

Publication No. US2005006955A1

GENERAL INFORMATION:

APPLICANT: PLAKSIN, DANIEL

APPLICANT: LEVANO, AVIGDOR

APPLICANT: SZANTON, ESTHER

APPLICANT: HAGAY, YOCHVED

APPLICANT: BEN-LEVY, RACHEL

APPLICANT: NISGAV, YAEI

APPLICANT: KANFI, YARIV

TITLE OF INVENTION: ANTIBODIES AND USES THEREOF

FILE REFERENCE: 10793-143

CURRENT APPLICATION NUMBER: US/10/880,922

CURRENT FILING DATE: 2004-06-30

PRIOR APPLICATION NUMBER: 60/484,061

PRIOR FILING DATE: 2003-06-30

NUMBER OF SEQ ID NOS: 64

SOFTWARE: PatentIn Ver. 3.2

SEQ ID NO 43

LENGTH: 18

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-10-880-922-43

Query Match 100.0%; Score 44; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YDYYPE 7

Db 9 YDYPPEE 15

RESULT 2
US-10-880-922-44

; Sequence 44, Application US/10880922
; Publication No. US20050069955A1
; GENERAL INFORMATION:

; APPLICANT: PLAKSIN, DANIEL

; APPLICANT: LEVANON, AVIGDOR

; APPLICANT: SZANTON, ESTHER

; APPLICANT: HAGAY, YOCHAVED

; APPLICANT: BEN-LEVY, RACHEL

; APPLICANT: NISGAV, YAEI

; APPLICANT: KANFL, YARIV

; TITLE OF INVENTION: ANTIBODIES AND USES THEREOF

; FILE REFERENCE: 10793-143

; CURRENT APPLICATION NUMBER: US/10/880,922

; CURRENT FILING DATE: 2004-06-30

; PRIOR APPLICATION NUMBER: 60/484,061

; PRIOR FILING DATE: 2003-06-30

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 44

; LENGTH: 18

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; FEATURE:

; NAME/KEY: MOD_RES

; LOCATION: (9)

; OTHER INFORMATION: Sulfated Tyr

US-10-880-922-44

Query Match 100.0%; Score 44; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YDYPPEE 7
Db 9 YDYPPEE 15

RESULT 3
US-10-880-922-50

; Sequence 50, Application US/10880922
; Publication No. US20050069955A1
; GENERAL INFORMATION:

; APPLICANT: PLAKSIN, DANIEL

; APPLICANT: LEVANON, AVIGDOR

; APPLICANT: SZANTON, ESTHER

; APPLICANT: HAGAY, YOCHAVED

; APPLICANT: BEN-LEVY, RACHEL

; APPLICANT: NISGAV, YAEI

; APPLICANT: KANFL, YARIV

; TITLE OF INVENTION: ANTIBODIES AND USES THEREOF

; FILE REFERENCE: 10793-143

; CURRENT APPLICATION NUMBER: US/10/880,922

; CURRENT FILING DATE: 2004-06-30

; PRIOR APPLICATION NUMBER: 60/484,061

; PRIOR FILING DATE: 2003-06-30

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 50

; LENGTH: 18

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; FEATURE: MOD_RES
; NAME/KEY: (12)
; LOCATION: (12)
; OTHER INFORMATION: Sulfated Tyr
US-10-880-922-50

Query Match 100.0%; Score 44; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YDYPPEE 7
Db 9 YDYPPEE 15

RESULT 4
US-10-880-922-57

; Sequence 57, Application US/10880922
; Publication No. US20050069955A1
; GENERAL INFORMATION:

; APPLICANT: PLAKSIN, DANIEL

; APPLICANT: LEVANON, AVIGDOR

; APPLICANT: SZANTON, ESTHER

; APPLICANT: HAGAY, YOCHAVED

; APPLICANT: BEN-LEVY, RACHEL

; APPLICANT: NISGAV, YAEI

; APPLICANT: KANFL, YARIV

; TITLE OF INVENTION: ANTIBODIES AND USES THEREOF

; FILE REFERENCE: 10793-143

; CURRENT APPLICATION NUMBER: US/10/880,922

; CURRENT FILING DATE: 2004-06-30

; PRIOR APPLICATION NUMBER: 60/484,061

; PRIOR FILING DATE: 2003-06-30

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 57

; LENGTH: 18

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; FEATURE:

; NAME/KEY: MOD_RES

; LOCATION: (11)

; OTHER INFORMATION: Sulfated Tyr

US-10-880-922-57

Query Match 100.0%; Score 44; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YDYPPEE 7
Db 9 YDYPPEE 15

RESULT 5
US-10-880-922-58

; Sequence 58, Application US/10880922
; Publication No. US20050069955A1
; GENERAL INFORMATION:

; APPLICANT: PLAKSIN, DANIEL

; APPLICANT: LEVANON, AVIGDOR

; APPLICANT: SZANTON, ESTHER

; APPLICANT: HAGAY, YOCHAVED

; APPLICANT: BEN-LEVY, RACHEL

; APPLICANT: NISGAV, YAEI

; APPLICANT: KANFL, YARIV

; TITLE OF INVENTION: ANTIBODIES AND USES THEREOF

; FILE REFERENCE: 10793-143

; CURRENT APPLICATION NUMBER: US/10/880,922

; CURRENT FILING DATE: 2004-06-30

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/ PRIOR APPLICATION NUMBER: 60/484,061
/ PRIOR FILING DATE: 2003-06-30
/ NUMBER OF SEQ ID NOS: 64
/ SOFTWARE: PatentIn Ver. 3.2
/ SEQ ID NO 58
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ NAME/KEY: MOD_RES
/ LOCATION: (9)_
/ OTHER INFORMATION: Sulfated Tyr
/ NAME/KEY: MOD_RES
/ LOCATION: (11)..(12)
/ OTHER INFORMATION: Sulfated Tyr
US-10-880-922-58
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Query Match          100.0%; Score 44; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 YDYYPPEE 7
Db 9 YDYYPPEE 15
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RESULT 6

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US-10-881-405-22
/ Sequence 22, Application US/10881405
/ Publication No. US20050152906A1
/ GENERAL INFORMATION:
/ APPLICANT: LEVANON, AVISDOR
/ APPLICANT: VOGEL, TIKVA
/ APPLICANT: PLAKSIN, DANIEL
/ APPLICANT: PERETZ, TUVIA
/ APPLICANT: AMIT, BOAZ
/ APPLICANT: COOPERMAN, LENA
/ APPLICANT: HAGAY, YOCHAVED
/ APPLICANT: SZANTON, ESTHER
/ APPLICANT: KANFI, YARIV
/ APPLICANT: BEN-LEVY, RACHEL
/ APPLICANT: SZRAUBER, TALIT
/ TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES
/ FILE REFERENCE: 10793/145
/ CURRENT APPLICATION NUMBER: US/10/881,405
/ PRIOR FILING DATE: 2004-06-30
/ PRIOR APPLICATION NUMBER: 60/484,235
/ PRIOR FILING DATE: 2003-06-30
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: PatentIn Ver. 3.2
/ SEQ ID NO 22
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: peptide
US-10-881-405-22
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Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 YDYYPPEE 7
Db 8 YDYYPPEE 14
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RESULT 7

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US-09-779-054-14
/ Sequence 14, Application US/09779054
/ Patent No. US20020120102A1
/ GENERAL INFORMATION:
/ APPLICANT: Lu, Xinjie
/ APPLICANT: Kakkar, Vijay
/ TITLE OF INVENTION: USE OF DENDROASPIN AS A SCAFFOLD FOR NON-DENDROASPIN DOMAINS
/ FILE REFERENCE: A-70312/TAL/AMS
/ CURRENT APPLICATION NUMBER: US/09/779,054
/ PRIOR FILING DATE: 2001-02-05
/ PRIOR APPLICATION NUMBER: GB 0002625.2
/ PRIOR FILING DATE: 2000-02-05
/ NUMBER OF SEQ ID NOS: 21
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 14
/ LENGTH: 66
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Modified dendroaspin (KGDW-dendroaspin-Gb)
US-09-779-054-14
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Best Local Similarity 100.0%; Pred. No. 4.7;
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QY 1 YDYYPPEE 7
Db 57 YDYYPPEE 63
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RESULT 8

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US-10-467-020-15
/ Sequence 15, Application US/10467020
/ Publication No. US20040072315A1
/ GENERAL INFORMATION:
/ APPLICANT: Lu, Xinjie
/ APPLICANT: VIK Kakkar, Vijay
/ TITLE OF INVENTION: Integrin-Binding Chimeras
/ FILE REFERENCE: 6613-66094
/ CURRENT APPLICATION NUMBER: US/10/467,020
/ PRIOR FILING DATE: 2003-08-01
/ PRIOR APPLICATION NUMBER: US 60/267,234
/ PRIOR FILING DATE: 2001-02-05
/ PRIOR APPLICATION NUMBER: PCT/GB02/00500
/ PRIOR FILING DATE: 2002-02-05
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 15
/ LENGTH: 66
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: Description of Artificial Sequence:
/ OTHER INFORMATION: Modified Dendroaspin (KGDW-dendroaspin-Gb)
US-10-467-020-15
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Query Match          100.0%; Score 44; DB 15; Length 66;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 YDYYPPEE 7
Db 57 YDYYPPEE 63
```

```
RESULT 9
US-10-068-426-10
/ Sequence 10, Application US/10068426
/ Publication No. US20030091576A1
/ GENERAL INFORMATION:
/ APPLICANT: Shaw, Gray D.
```

```

; APPLICANT: Sako, Dianne S.
; APPLICANT: Kumar, Ravindra
; APPLICANT: Sullivan, Francis
; APPLICANT: McDonagh, Tom
; TITLE OF INVENTION: Platelet Glycoprotein IB Alpha Fusion Polypeptides and
; FILE REFERENCE: 22058-503
; CURRENT APPLICATION NUMBER: US/10/068,426
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/266,838
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)..(290)
; OTHER INFORMATION: GPLB290
US-10-068-426-10
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Query Match          100.0%; Score 44; DB 14; Length 290;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 YDYYPEE 7
Db      276 YDYYPEE 282
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RESULT 10
US-10-068-426-11
; Sequence 11, Application US/10068426
; Publication No. US2003091576A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, Gray D.
; APPLICANT: Sako, Dianne S.
; APPLICANT: Kumar, Ravindra
; APPLICANT: Sullivan, Francis
; APPLICANT: McDonagh, Tom
; TITLE OF INVENTION: Platelet Glycoprotein IB Alpha Fusion Polypeptides and
; FILE REFERENCE: 22058-503
; CURRENT APPLICATION NUMBER: US/10/068,426
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/266,838
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)..(290)
; OTHER INFORMATION: GPLB290/2V
US-10-068-426-11
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Query Match          100.0%; Score 44; DB 14; Length 290;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 YDYYPEE 7
Db      276 YDYYPEE 282
```

```

RESULT 11
US-10-068-426-12
; Sequence 12, Application US/10068426
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; Publication No. US20030091576A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, Gray D.
; APPLICANT: Sako, Dianne S.
; APPLICANT: Kumar, Ravindra
; APPLICANT: Sullivan, Francis
; APPLICANT: McDonagh, Tom
; TITLE OF INVENTION: Platelet Glycoprotein IB Alpha Fusion Polypeptides and
; FILE REFERENCE: 22058-503
; CURRENT APPLICATION NUMBER: US/10/068,426
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/266,838
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)..(290)
; OTHER INFORMATION: GPLB290/1A
US-10-068-426-12
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Query Match          100.0%; Score 44; DB 14; Length 290;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 YDYYPEE 7
Db      276 YDYYPEE 282
```

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RESULT 12
US-10-382-758-10
; Sequence 10, Application US/10382758
; Publication No. US20030232047A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, Gray D.
; APPLICANT: Sako, Dianne S.
; APPLICANT: Kumar, Ravindra
; APPLICANT: Sullivan, Francis
; APPLICANT: McDonagh, Tom
; TITLE OF INVENTION: Platelet Glycoprotein IB Alpha Fusion Polypeptides and
; FILE REFERENCE: 22058-503
; CURRENT APPLICATION NUMBER: US/10/382,758
; PRIOR FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: US/10/068,426
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)..(290)
; OTHER INFORMATION: GPLB290
US-10-382-758-10
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Query Match          100.0%; Score 44; DB 15; Length 290;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 YDYYPEE 7
Db      276 YDYYPEE 282
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RESULT 13
US-10-382-758-11
; Sequence 11, Application US/10382758
; Publication No. US20030232047A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, Gray D.
; APPLICANT: Sako, Dianne S.
; APPLICANT: Kumar, Ravindra
; APPLICANT: Sullivan, Francis
; APPLICANT: McDonagh, Tom
; TITLE OF INVENTION: Platelet Glycoprotein IB Alpha Fusion Polypeptides and
; TITLE OF INVENTION: Methods of Use Thereof
; FILE REFERENCE: 22058-503
; CURRENT APPLICATION NUMBER: US/10/382,758
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: US/10/068,426
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/266,838
; PRIOR FILING DATE: 2001-02-06
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo sapiens
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; OTHER INFORMATION: GBLD290/2V
US-10-382-758-11

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RESULT 14
US-10-382-758-12
; Sequence 12, Application US/10382758
; Publication No. US20030232047A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, Gray D.
; APPLICANT: Sako, Dianne S.
; APPLICANT: Kumar, Ravindra
; APPLICANT: Sullivan, Francis
; APPLICANT: McDonagh, Tom
; TITLE OF INVENTION: Platelet Glycoprotein IB Alpha Fusion Polypeptides and
; TITLE OF INVENTION: Methods of Use Thereof
; FILE REFERENCE: 22058-503
; CURRENT APPLICATION NUMBER: US/10/382,758
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: US/10/068,426
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/266,838
; PRIOR FILING DATE: 2001-02-06
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)..(290)
; OTHER INFORMATION: GBLD290/1A
US-10-382-758-12
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RESULT 15
US-10-868-371-1
; Sequence 1, Application US/10868371
; Publication No. US2005008988A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, G. et al.
; TITLE OF INVENTION: PLATELET GLYCOPROTEIN IB ALPHA VARIANT FUSION
; TITLE OF INVENTION: POLYPEPTIDES AND METHODS OF USE THEREOF
; FILE REFERENCE: 22058-583
; CURRENT APPLICATION NUMBER: US/10/868,371
; CURRENT FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: 60/477,525
; PRIOR FILING DATE: 2003-06-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-868-371-1

Query Match          100.0%; Score 44; DB 17; Length 290;
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Db      276 YDYYPEE 282
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Job time : 106.75 secs

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